

#5

1 31  
 TCG ACT ATG AAT GAT GAT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC  
 ser thr met asn ala ~~asp~~ thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61 91  
 TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC  
 ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121 Cadherin  
 151 1xx EC motif xx|  
 AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC  
 arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181 211  
 CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC  
 leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241 271  
 AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA  
 ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301 331  
 ATC GCC GCC CTT CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT  
 ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361 391  
 GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA  
 asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421 451  
 GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG  
 gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

481 511  
 AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG  
 lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541 571  
 GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC  
 asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601 631  
 CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA  
 leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661 691  
 CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT  
 leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser

721 751  
 ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT  
 thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781 811  
 GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA GGG AAC GAC CGA TTT CCA  
 gly glu gly ala arg gly glu met met arg arg ala pro gly asn asp arg phe pro

841 871  
 GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG  
 gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

901 931  
 AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT  
 lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala  
 961 991  
 ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT  
 thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala  
 1021 1051  
 CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC  
 leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn  
 1081 1111  
 TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC  
 cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala  
 1141 1171  
 AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA  
 lys phe gly asp leu leu phe glu glu val glu gln cys phe asp leu cys his gln  
 1201 1231  
 GTC CTG CAC CAC TGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT  
 val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu  
 1261 1291  
 TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA  
 tyr leu leu met arg phe ser phe gly ala thr ser asp phe ala arg val lys met gln  
 1321 1351  
 GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG  
 val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu  
 1381 1411  
 AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT  
 arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr  
 1441 1471  
 CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA  
 pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr  
 1501 1531  
 GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT  
 val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile  
 1561 1591  
 GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG  
 ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu  
 1621 |xxxxxxxxxxxxxxxxxxxxxxxxxxxx transmembrane domain xxxxxxxx  
 AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG  
 lys his thr lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala  
 xxxxxxxxxxxxxxxxxxxxxxxx| 1711  
 TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC  
 leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val  
 1741 1771  
 AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG  
 ser phe gln asn ile ser ser asp val leu glu ser val val ser glu asp thr leu  
 1801 1831  
 TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC  
 ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly

1861 1891  
 CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG  
 leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921 1951  
 GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC  
 val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981 2011  
 ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG  
 thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041 |xxxxx ITAM xxxx| 2071  
 TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG  
 phe gly thr tyr phe arg val gly phe gly ser lys phe gly asp leu asp glu gln

2101 2131  
 GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG  
 glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2161 2191  
 GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT  
 ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro

2221 2251  
 GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC  
 val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2281 2311  
 TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC  
 tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2341 2371  
 CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT  
 arg arg phe met tyr thr pro phe thr leu glu gly arg pro arg gly glu leu his

2401 2431  
 GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC  
 glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2461 2491 |xxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
 AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA  
 arg ile ser val ile gln lys glu phe val leu thr pro ile glu val ala ile glu

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
 GAC ATG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA  
 asp met lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx| 2611  
 AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG  
 lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641 2671  
 GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC  
 glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2701 2731 |xxxxxxxxxxxxxx  
 AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA  
 asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
 AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT  
 asn lys arg leu ile thr ala asp gln arg glu tyr gln glu leu lys asn tyr

FIG. 1 (3 of 5)

xxx|  
 AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG  
 asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys  
 2881 2911  
 CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA  
 pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys  
 2941 2971  
 TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG  
 cys glu thr gln leu ser gln gly ser OCH glu lys pro ser ser phe val glu thr val  
 3001 3031  
 GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG  
 ala leu gln pro trp arg arg thr cys trp tyr leu lys asn gly thr phe ala thr gln  
 3061 3091  
 GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA  
 asp STP  
 3121 3151  
 TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG  
 3181 3211  
 GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC  
 3241 3271  
 AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA  
 3301 3331  
 TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA  
 3361 3391  
 AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC  
 3421 3451  
 TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA  
 3481 3511  
 AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA  
 3541 3571  
 ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA  
 3601 3631  
 CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG  
 3661 3691  
 CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG  
 3721 3751  
 CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA  
 3781 3811  
 AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT  
 3841 3871  
 CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT  
 3901 3931  
 TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT  
 3961 3991  
 GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA

FIG. 1 (5 of 5)

~7.5 kb —

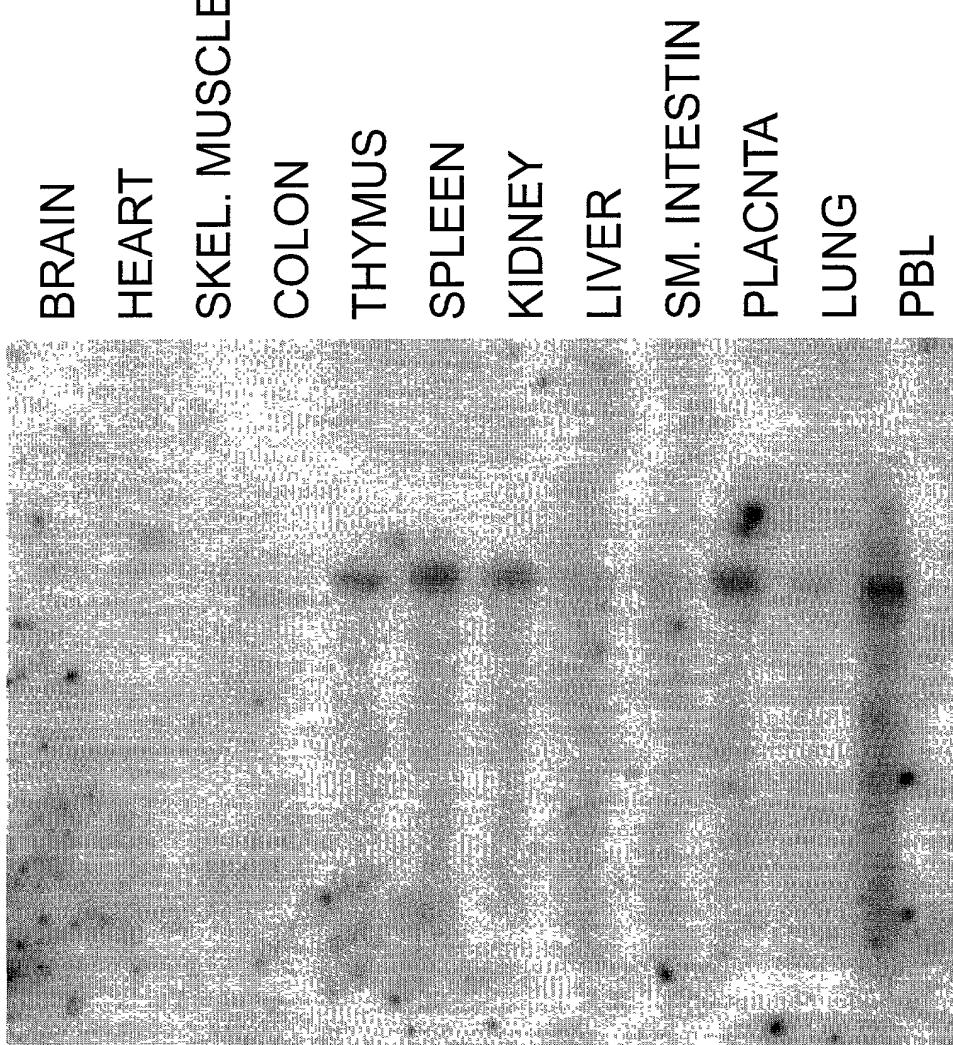


FIG. 2A

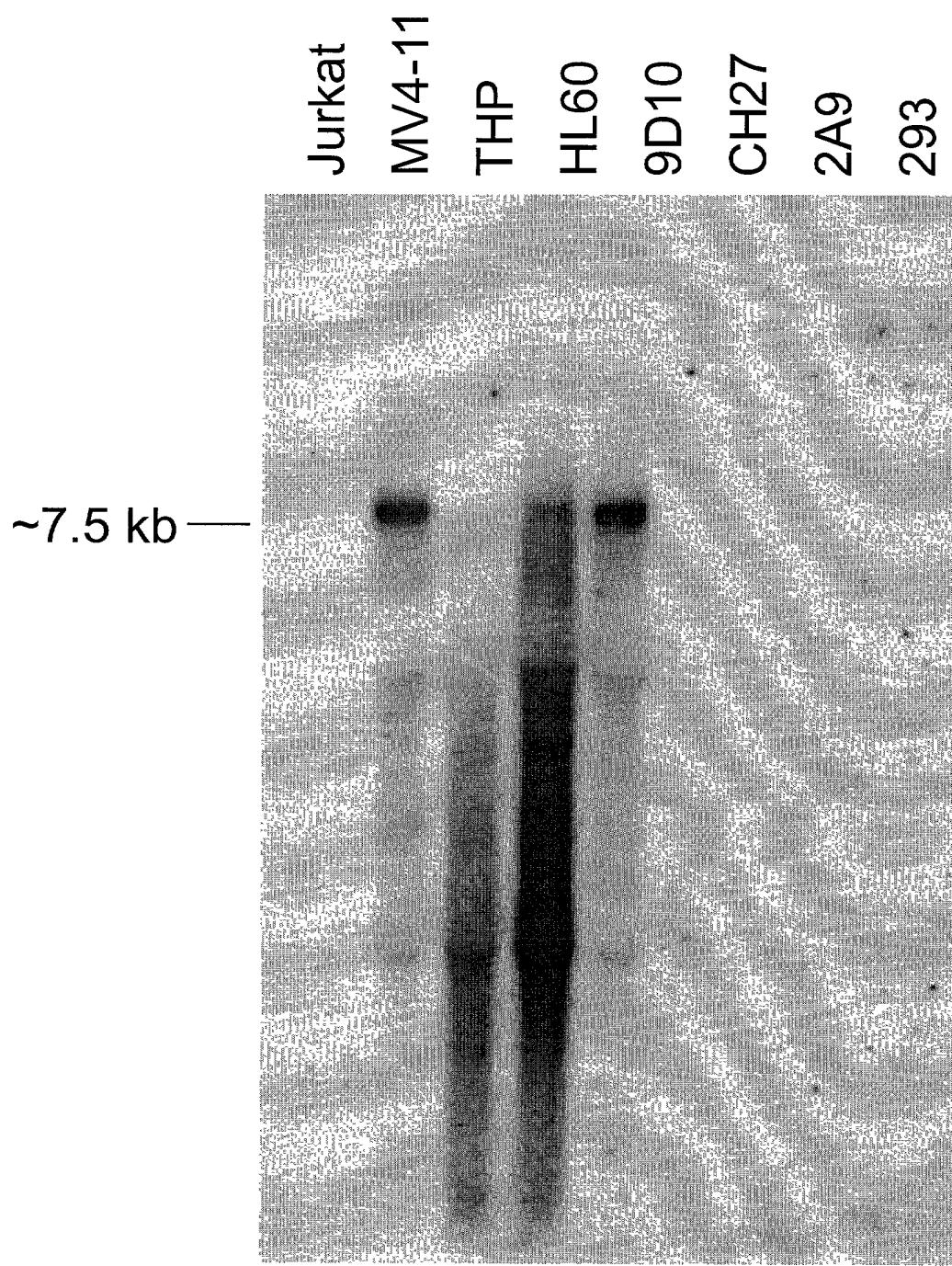


FIG. 2B

HC2A	ASGNLDKNARFSAIYRQDSNKLNSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
KIAA	-----
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
KIAA	-----
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	VLHHHQNPPEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPPEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHLLLTFHVSCDNSSKGSTKKRDUVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHLLLTFHVSCDNSSKGSTKKRDUVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-GPGPARSTVSISLISNSARV
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
	MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPVM
	MSFLPIIILNQLFKVLV-QNEEDEITTTVTRV
	NRSRSLSNSNPDISGTPPTSPDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES

FIG. 3A (1 of 5)

HC2A	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
KIAA	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
rat	-----
HC4	LFHIVSKCHEEGLDSYLSFIKYSFRPGKPSAPQAPIHETLATMMIALLKQSADFLAIN
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVHEDLAKNVTGLLK-SNDSPTVK
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP---TKKLFHEELALQWVVCVG--SVR---E
HC5	-----
Cadherin Cleavage	
HC2A	KLLRYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHAAETVVNMLMPHITQKFGD
KIAA	KLLKYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAETVVNMLMPHITQKFRD
rat	-----
HC4	KLLKYSWFFFELIAKSMATYLLEENKIKLTHGQRFPKAYHHALHSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFIAILKSMAQHLIDTNKIQLPRPQRFPESYQNELDNLVMVLSDHVIWKYKD
HC3	SALQQAWFFFELMVKSVMVHHLYFNDKLEAPRKSRFPERFMDDIAALVSTIASDIVSRFQK
HC5	-----
HC2A	NPEASKNAHSLAVFIKRCFTMDRGFVKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNAHSLAVFIKRCFTMDRGFVKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat	-----
HC4	IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1	ALEETRRATHSVARFLKRCFTMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFDL
HC3	DTEMVERLNTSLAFLNLLSVMMDRGFVFSLIKSCYKVSSKLYSLPNPSVLVSLRDFL
HC5	-----
HC2A	RVVCNHEHYIPLNLP-----PFGKGRIGR-----YQDLQL----DYSLTDEF
KIAA	RVVCNHEHYIPLNLP-----PFGKGRIGR-----YQDLQL----DYSLTDEF
rat	-----
HC4	QTICNHEHYIPLNLP-----AFAKPKLQR-----VQDSNL----EYSLSDAY
HC1	QEVCQHEHFIPLCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF
HC3	RIICSHHYVTLNLPCLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5	-----MNADTAPTPCPSIS--SQNSSCSSFQDQKIASMFRTSRVPA
Cadherin EC motif	
HC2A	CRNHFLVGLLLREVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA	CRNHFLVGLLLREVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat	-----
HC4	CKHHFLVGLLLRETSIALQDNYE---IRYTAISVIKNNLIKHAFDTRYQHKNQQAKIAQ
HC1	CRKHFLIGILLREVGFALQEDQD---VRHLALAVLKNLMAKHSFDDRYREPRKQAOIAS
HC3	RQQHYLAGIVLTELAVILDPAEGLFGLHKKVINMVHNLLSSHSDPRYSDPQIKARVAM
HC5	SSTS-SPGILFTELAAALDAESEGEGISEVQRKAVSAIHSLLSSHDLRPCVKPEVKVIAA
HC2A	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat	-----
HC4	LYLPFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEPCG----FTSP--AN--RGSL
HC1	LYMPLYGMLLDNMPRIYLKDLYPFTVNTSNOGSRDDLSTNGGFQSQTAIKHANSVDTFS
HC3	LYLPLIGIIMETVPQLYDFTETHNQRGRPICIATDDYESE-----SG--SMIS
HC5	LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA--GAIT

FIG. 3A (2 of 5)

HC2A	KDLLGAISGIAСПYTTSTPNINSVRNADSRGSLISTDGSNLSLPERNSEKSNSLDKHQQQSS
KIAA	KDLLGAISGIAСПYTTSTPNINSVRNADSRGSLISTDGSNLSLPERNSEKSNSLDKHQQQSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGIKREDSRGSLIP-EGATGFPDQGNTGEN-----TRQSS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
HC3	QTVAMAIAGTSPQ-----LTRPGSFLLTSTSGRQHT-----
HC5	QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----
HC2A	-----
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDFFTISEVCL
rat	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDFFTISEVCL
HC4	-----
HC1	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISETDLTLYWN-KVSPQELINILILLEVCL
HC3	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC5	-----TFSAESSRSLLICLWLKN-ADETVLQKWFTDLSVLQLNRLLDLYLCV
-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLFICV	
HC2A	-----
KIAA	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
rat	HQFQYMGKRYIAR-----TGM
HC4	-----
HC1	FHFRYMGKRNIARVHDAWLSKHFIDRKS-----QTMPALRNRSGVMM
HC3	QNFRYLGKRNIIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSREHGHK
HC5	SCFEYKGKKVFERMNSLTFK--KSKDMRAK-----LEEAIALGSIGARQEMV
-----LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR-----LEEAALLRGEGARGEMM	
HC2A	-----
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
HC4	-----
HC1	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVSS
HC3	QHRSQTLPIIRGK--NALSNPKL---LQMLDNTMTSNSNEIDIVHHVDTEANIATEGRG
HC5	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTEKLDKSRAEIEHEALIDGNLATEAN
-----RRRAPGNDRFP----GLNENLRWKKEQTHWRQANEKLDKTAELDQEALISGNLATEAH	
HC2A	-----
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLLY
rat	LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLLY
HC4	-----
HC1	KLSRGHSPLMKKVFDVYLCFLQKHQSEMAKLNVFTALRSLLY
HC3	LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC5	LTILDILVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNQSATALKHVFASLRLFVC
-----LIIILDTEIVVQTVS--VTE--KESILGGVLKVLLHSMACNQSAVYLQHCFATQRALVS	
-----LIIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCQSTTYLTHCFATLALIA	
HC2A	-----
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
rat	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC4	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC1	KFPSAFFKGRVNMCACAFCYEVLKCCCTS KISSTRNEASALLYLLMRNNFEYTKRKTFLRTH
HC3	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASASALLYLFMRKNFENFKQKSIVRSH
HC5	KFPFELLFEEETEQCADLCLRLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK
-----KFGDLLFEEEEEVQCFDLCHQVLHCCSSMDVTRSQACATLYLLMRFSFGATS--NFARVK	
HC2A	-----
KIAA	LQVIISVSQLIADVVGIGETRFQQSLSIINNCANSRDRLIKHTSFSSDVKDLTKRIRTVLM
rat	LQVIISVSQLIADVVGIGGTRFQQSLSIINNCANSRDRLIKHTSFSSDVKDLTKRIRTVLM
HC4	LQVIISLSQLIADVVGIGGTRFQQSLSIINNCANSRDRLIKHTSFSSDVKDLTKRIRTVLM
HC1	LQIIIIVSQLIADVALSGGSRFQESLFIIINNFANSDRPMLARAFPAEVKDLTKRIRTVLM
HC3	LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNFPAEVKDLTKRIRTVLM
HC5	MQVPMSSLSSLVGTSQNFNEEFLRRSLKTIILTYAEEDLELRETTFPDPQVQDLFVNLMILSS
-----MQVTMSSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTFPFTQVEELLCNLNSILY	

FIG. 3A (3 of 5)

Transmembrane

HC2A	ATAQMKEHENDPEMLVLDLQYSLAKSYASTPELRKTWLDSMARIHVVKNGDLSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVLDLQYSLAKSYASTPELRKTWLDSMARIHVVKNGDLSEAAMCYVHV
rat	ATAQMKEHENDPEMLVLDLQYSLAKSYASTPELRKTWLDSMARIHVVKNGDLSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLLIDLQYSLAKSYASTPELRKTWLDSMARIHVVKNGDFSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVLDLQYSLANSYASTPELRRTWLQNSMAKIHARNGDLSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLLIDLMYRIAKGYQTSPDLRLTLQNMAGKHSRSNHAEEAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMLYRIAKSYQASPDRLTLQNMMAEKHTKKCYTEAMCLVHA

SH3

HC2A	TALVAEYLTRKGV-----	FRQGCTAFRVITPN
KIAA	TALVAEYLTRKEA-----	VQWEPPPLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYLTRKEAD-----	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFLHRKKL-----	FPNGCSAFKKITPN
HC1	AALIAEYLKRKGYWVKEKICTASLLSEDTHPCDSNSLLTPSGGSMFSMGWPALFSITPN	
HC3	AALVAEYLSMLED-----	RKLPVGCVTFQNISSN
HC5	AALVAEYLSMLED-----	HSYLPVGSVSFQNISSN

ITAM

HC2A	I DEEASMMEDVGMD-----	VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIIP
KIAA	I DEEASMMEDVGMD-----	VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIIP
rat	I DEEASMMEDVGMD-----	VHFNEVDVLMELLEQCADGLWKAERLRLAGLTSINSSP
HC4	I DEEGAMKEDAGMM-----	VHYSEEVLLLEQCVCNGLWKAERYEIISEISKLIGPI
HC1	IKEEGAAKEDSGMH-----	TPYNENILVEQLYMCGEFLWKSERYELIADVNKPIIAV
HC3	VLEESAVSDDVVSPDEEGICSGKYFTESGLVGLLEQAAASFMSAGMYEAVNEVYKVIIIP	
HC5	VLEESVVSEDTLSPDEDGVCAQGYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIP	

ITAM ITAM ITAM ITAM

HC2A	YEKRRD-----	YEFKRDFERLAHILYDTIHRAYSKVTEVMHSGRLLGTYFRV	AFFGQAAQYQFTDSETDVE
KIAA	YEKRRDFERLAHILYDTIHRAYSKVTEVMHSGRLLGTYFRV	AFFGQAAQYQFTDSETDVE	
rat	SMKSGGTLETTTHLYDTIHRPYSKVTEVITR-----	A-----AGSWDLLPGGLFGQ	
HC4	YENRREFENLTQVYRTLHGAYTKTLEVMHTKKRLLG-----	TFFRVAFYQG	
HC1	FEKQRDFKFLSDLVYDIIHRSYLYKVAEVVNSEKRLFG-----	YYRVAFYQG	
HC3	HEANRDAKKLSTIHGKLQEAFSKIVHQSTGWERMF-----	TYFRVGFYG	
HC5	LEAHREFRKLTTHSKLQLRFDISVNKDH--KRMFG-----	TYFRVGFYGG	

ITAM

ITAM

HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRLLKIYSDKF	FGSENVKMIQDSGVNPKDLDKYA
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRLLKIYSDKF	FGSENVKMIQDSGVNPKDLDKYA
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRLLKIYSDKF	FGSENVKMIQDSGVNPKDLDKFA
HC4	SFFEEEDGKEYIYKEPKLTLGLSEISLRLVKLYGEK	FGTENVKIIQDSDKVNAKELDPKYA
HC1	GFFEEEEDGKEYIYKEPKLTLGLSEISQRLLKIYADK	FGADNVKIIQDSNKVNPKDLDPKYA
HC3	TKFGDLDEQEYVYKEPAITKLAEISHRLEGFYGERF	GEDVVEVIKDSNPVDCKLDPNKA
HC5	SKFGDLDEQEYVYKEPAITKLPEISHRLEAFYGCQ	GAEVFEVIKDSTPVDKLDPNKA

ITAM

HC2A	YIQTQVTHVIPFFDEKELEQERKTEFERSHNIRRFMFEMPFTQ	TGKROGGVEEQCKRRTILTA
KIAA	YIQTQVTHVIPFFDEKELEQERKTEFERSHNIRRFMFEMPFTQ	TGKROGGVEEQCKRRTILTA
rat	YIQTQVTHVTPFFDEKELEQERKTEFERCHNIRRFMFEMPFTQ	TGKROGGVEEQCKRRTILTA
HC4	HIQVTVYVKPYFDDKELEQERKTEFERHNISRFVFEAPY	TLGKQGCIEEQCKRRTILTT
HC1	YIQVTVYVPEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLD	GRAHTELHEQFKRKTI
HC3	YIQVTVYVPEPYFDTYEMKDRVTYFEKNFNLR	RFMYTTPFTLEGRPRGELHEQYRRNTVLTT
HC5	YIQVTVYVPEPYFDTYEMKDRVTYFEKNFNLR	RFMYTTPFTLEGRPRGELHEQYRRNTVLTT

FIG. 3A (4 of 5)

**Coiled-Coil 1**

HC2A	IHCFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA	IHCFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat	IHCFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
HC4	SNSFPYVKKRIPINCEQQINLKP	IDGATDEIKDKTAELQQLCSTSVDMDIQLQLKLQGSV
HC1	SHLFPYVKKRIPQVISQSSTELNP	IEVAIDEMSRKVSelnQLCTMEEVDMISLQLKLQGSV
HC3	SHAFPYIKTRVNVTKEEIIILTP	IEVAIEDMQKKTQELAFATHQDPADPKMLQMVLQGSV
HC5	MHAFFPYIKTRISVIQKEEVLTP	IEVAIEDMKKKTLQLAVAINQEPPDAKMLQMVLQGSV

**Coiled-Coil 2**

HC2A	SVQVNAGPLAYARAFLDDDTNTKRYPDNKVKLLKEVFRQFVEACGQA	ALAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLDDDTNTKRYPDNKVKLLKEVFRQFVEACGQA	ALAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLDDDTNTKRYPDNKVKLLKEVFRQFVEACGQA	ALAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLNDSQASKYPPKKVSELKDMFRKF	IQACSIALELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLLEETNAKKYPDNQVKLLKEIFRQFADACGQ	ALDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFDKFTKRCEDALRKNKSLIGPVQKE	
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEA	VEKNKRLITADQRE

**Coiled-Coil 2**

HC2A	YQEEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPTSTMVHGMTSS	
KIAA	YQEEEMKANYREMAKELSEIMHEQLG-----	
rat	YQEEEMKANYREIRKELSDIIVRIPGEDKRATKFP AHLQRHQ RDTNKHSGSRVDQFILS	
HC4	YHEGLKSNFRDMVKELSDIIHEQILQEDTMHSPWMSNTLHVFC	AIISGTSSDRGYGSPRYA
HC1	YQEELRSHYKDMSELSTVMNEQITGRDDLSK--RGVDQTCTRISKATPALPTVSISS	
HC3	YQRELG---KLSS-----P-----	
HC5	YQQELKKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS--	

**PBM**

HC2A	SSVV-----	
KIAA	-----	
rat	CVTLPHPHVGTCFVMCKLRTTFRANHWF	CQAQEEAMGNGREKEPWTVIFNSRFYRSWGK
HC4	EV-----	
HC1	SAEV-----	
HC3	-----	
HC5	-----	

HC2A	-----	
KIAA	-----	
rat	VHIFF	
HC4	-----	
HC1	-----	
HC3	-----	
HC5	-----	

**FIG. 3A (5 of 5)**

			C
TRG	PKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDKFAYI	YI	QVTHVTPFFFDEKE
CLASP-1	PKLTGLSEISQRLLKLYADKFGADNVKIIQDSNKVNPKDLDPKAYI	YI	QVTYVTPFFFKE
CLASP-2	PKLTPLSEISQRLLKLYSDKFGSENVKMTQDSGKVNPKDLDKFAYI	YI	QVTHVTPFFFDEKE
CLASP-4	PKLTGLSEISLRLVKKLYGEKFGTENVKIIQDSDKVNAKELDPKYAH	I	QVTVVKPYFDDKE
CLASP-3	PAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDCKLDPNKAYI	QI	ITYVEPYFDTYE
KIAA0716	HDYERLEAFQQRMLNEFPHAIA-----MQHANQPDETIFQAAQY	LQI	YAVTPIPESQE
DOCK3	HDYERLEAFQQRMLSEFPQAVA-----MQHPNHPDDA1LQCDAAQY	LQI	YAVTPIPDYVD
DOCK2	FQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGQYI	QCF	TCVQPVLDDEHP
DOCK180	EYERREDFQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGQYI	QCF	TCVQPVLDDEHP
CONSENSUS	L L Y M F	YI Q+ V P D L E	

	D		E
CLASP-1	RTILTSHLF	FPVKKRIQV	PIEVAIDEMSRKVSELN
TRG	RTILT	TAIHC	FPVVKKRI
KIAA1058	RTILT	TAIHC	FPVVKKRI
CLASP-2	RTILT	TAIHC	FPVVKKRI
CLASP-6	RTILT	TAIHC	FPVVKKRI
CLASP-4	RTILT	TSNSF	PPVKKRIP
CLASP-3	KTILT	TSNSF	HPYIKTR
CLASP-5	NTVLT	TMHAF	HPYIKTR
KIAA0716	RTSLYL	VQSLPGI	SRWF
DOCK2	RTSFV	TAYKLPGI	EVKREV
DOCK3	RTT	LTLSLPGI	VHMSQTT
DOCK180	RTSFV	TAYKLPGI	PLENA
CONSENSUS	RT L	FP V + V	AIETM
			STANEKIL
	F	L L	+
			I

FIG. 3B (1 of 2)

CLASP-1	SLQLKLOGSVSVKVNVAGPMA	YARAFLEE	TNAKKYPDNQV--KIL	KEIFRQFADACGQALD
TRG	KLQLKLOGSVSVQVNAGPLA	YARAFLDD	TNTKRYPDNKV--KIL	KEVFRQFVEACGQALA
KIAA1058	KLQLKLOGSVSVQVNAGPLA	YARAFLDD	TNTKRYPDNKV--KIL	KEVFRQFVEACGQALA
CLASP-2	KLQLKLOGSVSVQVNAGPLAYARAFLDD	TNTKRYPDNKV--KIL	KEVFRQFVEACGQALA	
CLASP-6	KLQLKLOGSVSVQVNAGPLAYARAFLDD	TNTKRYPDNKV--KIL	KEVFRQFVEACGQALA	
CLASP-3	MLQMVLQGSVGTTVNQGLEVAQVFLSE	--IPSDPKLFRHHNKIRLCFKDFTKRCEDALR		
CLASP-4	QLQLKLOGCVSVQVNAGPLAYARAFLND	SQASKYPPKKVSELKDMFRKFI--QACSTALE		
CLASP-5	MLQMVLQGSVGTAVNQGLEVAQVFLAE	--IPADPKLYRHHNKIRLCFKEFIMRCGEAVE		
KIAA0716	PLTMCLNGVIDAAVNGGVSRYQEAFFVKEYIILSHPEDGEKIAARIRELMLEQAQILEFGLA			
DOCK2	PLSMLLNGIVDPAVMGGFAKYEKAFFTEEYVVRDHPEDQDKLTHIKDLIAWQIPFLGAGIK			
DOCK3	LLSMCLNGVIDAAVNGGIARYQEAEFFDKDYINKHPGDAEKITQELMQUEQVHVLGVGLA			
DOCK180	PLSMLLNGIVDPAVMGGFAKYEKAFFTEEYVVRDHPEAHEKIEKIKDLIAWQIPFLAEGIR			
CONSENSUS	L M L+G V VN G Y AFL + + P L+			L
	L I V V F +			I

DOCK2=KIAA0209

DOCK3=KIAA0299

CLASP2variant=KIAA1058

FIG. 3B (2 of 2)

ref 1.1

1 31  
TCG ACT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC  
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61 91  
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC  
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121 151  
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC  
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181 211  
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC  
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241 271  
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA  
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301 331  
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT  
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361 391  
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA  
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421 451  
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG  
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asp leu

481 511  
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG  
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541 571  
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC  
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601 631  
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA  
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661 691  
CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT  
leu phe ile cys val leu cys phe glu tyr lys gln ser ser asp lys val ser

721 751  
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT  
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781 811  
GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA GGG AAC GAC CGA TTT CCA  
gly glu gly ala arg gly glu met met arg arg ala pro gly asn asp arg phe pro

841 871  
 GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG  
 gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu  
  
 901 931  
 AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT  
 lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala  
  
 961 991  
 ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT  
 thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala  
  
 1021 1051  
 CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC  
 leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn  
 ↓ ref 3.1  
 1081 1111  
 TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC  
 cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala  
  
 1141 1171  
 AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA  
 lys phe gly asp leu leu phe glu glu val glu gln cys phe asp leu cys his gln  
  
 1201 1231  
 GTC CTG CAC CAC TGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT  
 val leu his his ser ser ser met asp val thr arg ser gln ala cys ala thr leu  
  
 1261 1291  
 TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA  
 tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln  
  
 1321 1351  
 GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG  
 val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu  
  
 1381 1411  
 AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT  
 arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr  
  
 1441 1471  
 CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA  
 pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr  
  
 1501 1531  
 GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT  
 val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile  
  
 1561 1591  
 GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG  
 ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu  
  
 1621 1651  
 AAA CAC ACC AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCG GCT GCG  
 lys his thr lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala

FIG. 4A (2 of 7)

1681 1711  
 TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC  
 leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val  
  
 1741 1771  
 AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG  
 ser phe gln asn ile ser ser asn val leu glu glu ser val val ser glu asp thr leu  
  
 1801 1831  
 TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC  
 ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly  
  
 1861 1891  
 CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG  
 leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu  
  
 1921 1951  
 GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC  
 val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu  
  
 1981 2011  
 ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG  
 thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met  
  
 2041 2071  
 TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG  
 phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln  
  
 2101 2131  
 GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG  
 glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu  
  
 2161 2191  
 GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT  
 ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro  
 ref 4.1  
  
 2221 2251  
 GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC  
 val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro  
  
 2281 2311  
 TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC  
 tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu  
  
 2341 2371  
 CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT  
 arg arg phe met tyr thr pro phe thr leu glu gly arg pro arg gly glu leu his  
  
 2401 2431  
 GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC  
 glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr  
  
 2461 2491  
 AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA  
 arg ile ser val ile gln lys glu glu phe val leu thr pro ile glu val ala ile glu

FIG. 4A (3 of 7)

2521 2551  
 GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA  
 asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala  
  
 2581 2611  
 AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG  
 lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu  
  
 2641 2671  
 GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC  
 glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his  
  
 2701 2731  
 AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA  
 asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys  
  
 2761 2791  
 AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT  
 asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys asn tyr  
  
 2821 2851  
 AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG  
 asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys  
  
 2881 2911  
 CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA  
 pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys  
  
 2941 2971  
 TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG  
 cys glu thr gln leu ser gln gly ser OCH  
 ref 5.1  
  
 3001 3031  
 ↓ GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG  
  
 3061 3091  
 GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA  
  
 3121 3151  
 TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG  
  
 3181 3211  
 GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC  
  
 3241 3271  
 AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA  
  
 3301 3331  
 TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA  
  
 3361 3391  
 AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC  
  
 3421 3451  
 TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

FIG. 4A (4 of 7)

3481 3511  
 AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA  
 3541 3571  
 ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA  
 3601 3631  
 CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG  
 3661 3691  
 CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG  
 3721 3751  
 CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA  
 3781 3811  
 AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT  
 3841 3871  
 CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT  
 3901 3931  
 TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT  
 3961 3991  
 GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA  
 4021  
 AAC TCG

### Ref 1.1

Sequence of BAC19 using primer HC5S11, which spans nucleotides 3-22 of the cDNA. Exon sequence is underlined and represents nucleotides 32-57.

CTCTCTGTCTTCATATCTTCCAGGTTATAAAGNATTTTACTAAAAGAANATTCA  
 NGCTATTTCATTTAACTAGCTCAGTTAACATGTATTCCCTATAAAGGTTAGTCTTATTAA  
 ATTGACAAAACAATCAAACAAATTCAAACCCAGATCAAGTATGCTACCCCTGAAGGTTACACC  
 ACTAGCTAAGAATTAAACAACTAAGTAATTGGTTCTCCCCCAGGCTCAAGGCTCCCTGA  
 TCAGGTTAAGTAAAGCCAAGAATCCAATAAGCCCTATGAAATTAGAAACTCATAGAA  
 AAGTCTCAAATCTTCTGCTGACATTAGCCAATTGTTATTATGCAAATAGAGGATT  
 NCAAGTAAATAAGTTGGAACCTGTTACCAGGTTTGCGAGCAGNCCTCTAAGAGCTT  
 AACTGGTCATGCATTGAATGCCGAGAGCAAAGAGGAATGGAGAGGGNTGTAAGNGG  
 TTCCAATNTTACTGGAACCCACCATCTTNGAAGTCTGATACTTAACTGNGTGT  
 GNCTCTTCTGTTCTGTCNGCAAGNAG  
 TGCCTATGAAA

Ref 2.1

Sequence of BAC19 using primer HC5AS10b, which spans nucleotides 560-580 of Exon sequence is underlined and represents nucleotides 510-553.

TGCGAGTAGTGTCCCGTTCAGCATGTTACTGCTTATAGGGCTGAAGGGAGGCACG  
ATTGGGGATGGAGGCCAGGGAAAGAAGTCACAGAACAGAAAAATTGAGGCTTAACA  
GTCAAGCAACAGAAAAATTCAAAGTGTCTCTTAAACATGACTGTACATCACTG  
CTAGGCTGGAGATCTATTGCCAGTAGCCCTGCCTCCCTAGGCAGGGAAAGCTGTGTT  
CTTGAGTAGCGCTACTCAGCAAAGAGGCTCACCTGGGCAGTATTGAGCTAGGTT  
TCAGCCACCGTATCTGAGTACCTCTGTCTTANGAGCAGTGTGGCCTGGTATCACCCCT  
GGGCCTTGATCATGCGTGCTGCAATCCCAGTGATACAAAGAGGCTTCATGCTGCTAA  
GATCTCCAAGTATTCTCCTCGTGTGGCAGCAGAGGGTTAGACTNCAGGGAGA  
AGGAAACTGGCTGGGTGCCATGAATAANCTGCTGTTCAAGANTTAACCTTTGTTAC  
ATAAGNGCAAAGGTATAACATAAAGGGNCATGAACGCTAACNAAATTNATCAAAT  
CCATGTTGGGAGTTCTTGTNATNGGAAGTTAACCCCTAA

Ref 3.1

Sequence of BAC13 using primer C5S3, which spans nucleotides 1086-1105 of the cDNA. Exon sequence is underlined and represents nucleotides 1110-1120.

CCCNGCTTTGGCAANGTAANCTGGGATGCTTGTTCCTCTTAATTAAAGAG  
NAAGANTTTTAGCTTCATACTTCTCTTCAGGGGACCAAAAGTCACAGAGCATA  
TTAAGTGGCANAACCCNAAGGTCTTAAGTCTCCTAGGAAGAAAGCAGATGCCCTGA  
TTCTGTGGGAAGCCACCATGGAGAGGAAAAGCAGTGGCTCCCATATTGAAGTGNGGA  
CTTAACCTCTAGAAAGTTAAAANGGCCATTGCTGAAGGGCTATGACATGAGAACAGA  
GATCAACTGAGTGACTTAGCAANTCCTACTCTCTGTAAANACCTCTGGTGAGTGAGA  
NTAAATCCTNTATGTGACGCCATTAGTCTTACAAAANGTCATGCCNTAAAATGCCAN  
GAAGGNAGAAATGAATTCTCACGCCNGAGGAATGAGGATTATNCTGGGGGACA  
TGCANAAATATTNNNCCCCNATTATTNATTATTGAGACNGAGTNTCGNT  
CTAATGCCCTCAGGCTGGNAGGTGGNAGGTGGTCCCATTNAANCTTANNTNGGA  
AGGNCTCTTGNGCCCCNGGGGNGNAAAGNGAATTCCCTAAATGCCTNCANNCCC  
TCCCTGGANGTTATTGGGGNNTNTAAAGGGCNGTGGCNG

Ref 4.1

Sequence of BAC13 using primer C5S7, which spans nucleotides 2196-2205 of the cDNA. . Exon sequence is underlined and represents nucleotides 2225-2231.

ACAAAAAACTAACCATCANTCTAAATCCAAACANCTTTTAAGAATACCTAANG  
AGCTCAACNAGGGGACTNTCCAANGCACTTAAATGCAGNCAAACNACNNCAAG  
AGNGGCAACTACTAATGGGCANATCTNAAAGAAAATAGNCAAAGGNNGGAATCA  
TAATAGGAGCNACCACCTTANGAACCAACTGGGACCTGGAACGNATNAGGNCC  
TCTACATACATCATNNNATANCATCCTGCAACGACCCCTGGAAGGAGANAGANGNA  
TTCCTANNNTAGAGANGAGANAACGGGACATGGGAAGAGGNAAGCGAAGGGTTCA  
AGGGGANGNAAGCGAGCAGANCCAGGGNCTCANACTNGNGGGNNTGGGGGNTN  
CTGNNNCCCTACNCTNGNANGAACAGNGNNTTGANNTGGCTTNGANTA

Ref 5.1

Sequence of BAC13 using primer 122047F1, which spans nucleotides 3537-3556 of the cDNA. Exon sequence is underlined and represents nucleotides 3000-3492.

This region does not contain a intron in this region

FIG. 4A (6 of 7)

CCANNAGATTNTTGNAACGNNGTAGGCTTCTTGTAGATTATTGAAAATGTTCGT  
ACTTCTACAAGTTGCCCTGCCTCCTATAAAGAGTGAAANTCANTTGAATCGACTGG  
TGGATAATTNTTCCATTTCCTCAGGCAATTNGAGTTACTCCAATAAATTCAAATAT  
GGGCCAGAGGAAATCATCTTCAGATGGCAGTGATTGCCAGTCAGCAGGAGAAC  
TGCTTATGCCTTGTGTTGGTACATTGTGGAAAAACACACTTTAATAAACAGCANTCATG  
CCTGAGTACCCATCCTCCATCCCGCCACCCCCCAGTATGGCAAAATCTGGTCAGAGT  
CCATTGGGAATAATTCCATGGTCCTGGGATCCCAAAGCTCCAGAAGTGCTGGCTG  
ATCAANGGAGTGTACAGTCAGTCCTGGTGGCAAAATGTCCCATTTTAAGTACCA  
AGCAAAGGTTCTTCTTNCAAGGTTNCTAGGCC

FIG. 4A (7 of 7)

FIG. 4B (1 of 5)

Refs

HC2A IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN  
 KIAA IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN  
 rat -----

HC4 LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLHETLATMMIALLKQSADFLAIN  
 HC1 LPDIVAKCHEEQLDHQSVDQSYIKFVFKTR---ACKERPVHEDLAKNVGQLL-SNDSPTVK  
 HC3 TQAMDRSCNRMSSHTETSSFLQTLTGRLP---TKKLFHEELALQWVVCSSG--SVR---E  
 HC5 -----

Cadherin  
Cleavage

HC2A KLLRYSWFFFDVLIKSMAQHLENSKVKL[RNQRFPASYYHAAETVVNMLMPHITQKFGD  
 KIAA KLLKYSWFFFDVLIKSMAQHLENSKVKL[RNQRFPASYYHAAETVVNMLMPHITQKFRD  
 rat -----

HC4 KLLKYSWFFFETIAKSMATYLLEENKIKLTHGQRFPKAYHHALHSLFLAIT-IVESQYAE  
 HC1 HVLKHSWFFFETIAKSMATYLLEENKIKLTHGQRFPKAYHHALHSLFLAIT-IVESQYAE  
 HC3 SALQQAWFFFELM/KSMVHHLYFNDKLEAPRKSRFPERFMDDIAALVSTIASDIVSRFQK  
 HC5 -----

HC2A NPEASKNANHSLAVFIKRCFTMDRGFVFKQIN--NYIS--CFAPGDPKTLFEYKFEFL  
 KIAA NPEASKNANHSLAVFIKRCFTMDRGFVFKQIN--NYIS--CFAPGDPKTLFEYKFEFL  
 rat -----

HC4 IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN--DYIS--GFSPKDPKVLAEYKFEFL  
 HC1 ALEETRRATHSVARFLKRCFTMDRGCVFKMVN--NYIS--MFSSGDLKTLQYKFDL  
 HC3 DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVIVSILRDFL  
 HC5 -----

HC2A RVVCNHEHYIPLNLPM----PFGKGRQR-----YQDLQL---DYSLTDEF  
 KIAA RVVCNHEHYIPLNLPM----PFGKGRQR-----YQDLQL---DYSLTDEF  
 rat -----  
 HC4 QTICNHEHYIPLNLPM----AFAKPKLQR-----VQDSNL---EYSLSDEY  
 HC1 QEVCQHEHFIPFLCPLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF  
 HC3 RIICSHEHYVTLNLPCSLTPASPSPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF  
 HC5 -----MNADTAPTPCPSIS--SQINSSSCSSFQDQKIASMFDRTSRVPA

1.1

Cadherin  
EC motif

HC2A CRNHFLVGILLREVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT  
 KIAA CRNHFLVGILLREVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT  
 rat -----  
 HC4 CKHHFLVGILLRETSIALQDNYE---IRYTAISVIKNLLIKHAFDTRYQHKNQQAKIAQ  
 HC1 CRKHFLIGILLREVGVFALQEDQD---VRHLALAVLKNLMAKHSFDDRYREPRKQAAQIAS  
 HC3 RQHYLAGIVLTELAVILDPDAEGLFGLHKKVINMVHNLLSSHDSPRYSDPQIKARVAM  
 HC5 SSTS-SPGILLFTELAAALDAEGERGISEVQRKAVSAIHSLLSSHDLPRCVKPEVKVIAA

HC2A LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH  
 KIAA LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH  
 rat -----  
 HC4 LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH  
 HC1 LYLPFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG---FTSP--AN--RGSL  
 HC3 LYMPLYGMLLDNMPRIYKLKDLYPFTVNTSMQGSRDDLSTNGGFQSQTAIKHANSVDTFS  
 HC5 LYLPPLIGIIMETVPQLYDFTETHNQRGRPICIATDDYESE---SG---SMIS  
 LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE---GA---GAIT

FIG. 4B (2 of 5)

Refs

HC2A	KDLLGAISG ASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDK HQQSS	2.1
KIAA	KDLLGAISG ASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDK HQQSS	
rat	-----	
HC4	TDKDTAYGSFQNG-----HGIKREDSRGSLIP-EGATGFPDQGNTGEN-----TRQS	
HC1	KDVLNSIA AFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL	
HC3	QTVAMAIAGTSPQ-----LTRPGSFLLTS TSGRQHT-----	
HC5	QNVNALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----	
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSSDALFTYWN-KASTSELMDFFTISEVCL	2.1
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSSDALFTYWN-KASTSELMDFFTISEVCL	
rat	-----	
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMIEDTLLTYWN-KVSPQELINILILLEVCL	
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSII DVCL	
HC3	-----TFSAESSRSLLICLLWVLKN-ADETVLQKWFDTLSVLQLNRLLDLLYLCV	
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV	
HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM	2.1
KIAA	HQFQYMGKRYIAR-----TGMM	
rat	-----	
HC4	FHFRYMGKRNIARVHDAWLSKHFGRDRKS-----QTMPALRNRSGVM	
HC1	QNFRYLGKRNIAIRKIAAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSREGHK	
HC3	SCFEYKGKVFERNMSLTFK--KSKDMRAK-----LEEAIALGSIGARQEMV	
HC5	LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR-----LEEAALLRGEGARGEADM	
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	2.1
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
rat	-----	
HC4	QARLQHL-----SSLESS-----FTLNHSSTTEADIFHQALEGNTATEVS	
HC1	QHRSQTLPIIRGK--NALSNPKL---LQMLDNTMTSNSNEIDIVHHVDTENIATEGC	
HC3	RRSRGQIERSPSGSAGFSQENLRWRKDMTHWRQNTEKLDKSRAEIEHEALIDGNLATEAN	
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTAELDQEALISGNLATEAH	
HC2A	LTALDTLSLFTLAFK NQLLADHGHNPLMKVFDVYLCFLQKHQSE TALKNVFTALRS LIY	3.1
KIAA	LTALDTLSLFTLAFK NQLLADHGHNPLMKVFDVYLCFLQKHQSE TALKNVFTALRS LIY	
rat	-----KLSRGHSPLMKVFDVYLCFLQKHQSE MALKNVFTALRS LIY	
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPPLMKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS	
HC1	LTILDLVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNQSATALKHVFA SRLFVC	
HC3	LIILDTLEIVVQTVS--VTE S--KESILGGVVLKVLHSMACNQS A VY LQHCFATQRALVS	
HC5	LIILDMQENI IQASS--ALDC--KDSLLGGVVLVLSNLCDQSTTYLTHCFATLALIA	
HC2A	KFPSTFYEGRADMCALCYEILKCCNSKLSSIRTEASQILYFLMRNNFDYTGKKS FVRTH	3.1
KIAA	KFPSTFYEGRADMCALCYEILKCCNSKLSSIRTEASQILYFLMRNNFDYTGKKS FVRTH	
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQILYFLMRNNFDYTGKKS FVRTH	
HC4	KFPSAFFKGRVNMC AAFCYEVLKCCCTS KISSTRNEASALLYLLMRNNF EYTKRKTFLRTH	
HC1	KFPSAFFQFGPADLCGSFCYEVLKCCNHSRSRSTQTEASALLYLFMRKNF EFNKQKSIVRSH	
HC3	KFPELLFEEETEQCADLCLRLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK	
HC5	KFGDLLFEEVEQCFDLCHQVLHHCSSMDVTRSQACATLYLLMRFSFGATS--NFARVK	
HC2A	LQVIISVSQLIADVVGIGETRFQQSLSIINNCANS DR LIKHTSFSSDVKDLTKRIRT VLM	3.1
KIAA	LQVIISVSQLIADVVGIGETRFQQSLSIINNCANS DR LIKHTSFSSDVKDLTKRIRT VLM	
rat	LQVIISLSQLIADVVGIGGTRFQQSLSIINNCANS DR LIKHTSFSSDVKDLTKRIRT VLM	
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINNFANS DR PMLARAFPAEVKDLTKRIRT VLM	
HC1	LQIIIAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKN\$NFPAEVKDLTKRIRT VLM	
HC3	MQVPMISLSSLVGTSQNFNEEFLRRSLKTIILTYA EEDLELRETTFPDQVQD L VFNLH MILS	
HC5	MQVPMISLSSLVGTSQNFNEEFLRRSLKTIILTYA EEDLELRETTFPDQVQD L VFNLH MILS	

FIG. 4B (3 of 5)

### Transmembrane

## Refs

HC2A	ATAQMKEHENDEMLVLDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
KIAA	ATAQMKEHENDEMLVLDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
rat	ATAQMKEHENDEMLVLDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLDSMAKIHVKNGDFSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLIDLQYSLANSYASTPELRRRTWLQESMAKIHARNGDLSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPDLRLLTWLQNMAGKHSERSNHAAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASPDRLTWLQNMMAEKHTKKCYTEAMCLVHA

	SH3		
HC2A	TALVAEYLTRKGV		-FRQGCTAFRVITPN
KIAA	TALVAEYLTRKEA	-VQWEPPPLLPHSHSACLRRS	RSGGVFRQGCTAFRVITPN
rat	TALVAEYLTRKEAD	-LALQREPPVFVPSHTSCQRKSR	SGGMFRQGCTAFRVITPN
HC4	AALVAEFLHRKKL		-FPNGCSAFKKITPN
HC1	AALIAEYLKRKGYWKVEKIGT	ASLLSEDTHPCDNSLLTTPSGG	SMFSMGWPALFSITPN
HC3	AALVAEYLSMLED		-RKYLPVGCVTFQNISSN
HC5	AALVAEYLSMLED		-HSYLPVGSVSFQNISSN

ITAM  
IDEEASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIP  
IDEEASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIP  
IDEEASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP  
IDEEGAMKEDAGMMD-----VHYSEEVILLEQCVCNGLWKAERYEIISEISKLIGPI  
IKEEGAAKEDSGMH-----TPYNENILVEQLYMCGEFLWKSERIYELIADVNPPIIAV  
VLEESAVSDDVVSPDEEGICSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLIPI  
VLEESVVSDEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLIPI

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-			
KIAA	YEKRRDFERLAH	LYDTIHRAYSKVTEVMHSGRLLG	TYFRV	AFFGQAAQYQFTDSETDVE
rat	SMKSGGTLETTH	LYDTIHRPYSKVTEVITR	-A	AGSWDLLPGLFGQ
HC4	YENRREFENLTQVYRTI	HGAYTKILEVMHTKKRLG	-	TFFRVAFYQG
HC1	FEKQRDFKKLSDLYYD	IHRSYLKVAEVVNSEKRLFG	-	RYYRVAFYQG
HC3	HEANRDAKKLSTIHGKLQEAFSKIVHQ	STGWERMFG	-	TYFRVGFYG
HC5	LEAHREFRKLTLTHSKLORAFDSIVNKDH	-KRMFG	-	TYFRVGFYGG

	ITAM	ITAM
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGVNPKDLDKYA	
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGVNPKDLDKYA	
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGVNPKDLDKYA	
HC4	SFFEEEDGKEYIYKEPKLTGLSEISLRLVKLGYGEKFGTENVKIIQDSDKVNAKELDPKYA	
HC1	GFFEEEKGKEYIYKEPKLTGLSEISQRLLKLYADKFGADNVKIIQDSNKVNPKDLDPKYA	
HC3	TKFGDLDEQFVYKEPAITKLAIESHRIE <del>Q</del> FYGERFGEDVVEVIKDSNPVDKCKLDPNKA	
HC5	SKFGDLDEQFVYKEPAITKLPYEISHRLEAFYQGCFGAEFVEVIKDSTPVDK <del>T</del> KLDPNKA	

FIG. 4B (4 of 5)

**Coiled-Coil 1**

HC2A	IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA	IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat	IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV
HC4	SNSFPYVKKRIPINCEQQINLKPIDGATDEIKDKTAELQQLCSSTDVDMIQLQLKLQGSVW
HC1	SHLFPYVKKRIPQVISQSSTELNPIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3	SHAFPYIKTRVNVTKEEIIILTPIEVAIEDMOKKTOELAFATHQDPADPKMLQMVLOGSV
HC5	MHAFPYIKTRISVIQKEEFVLTPIEVAIEDMKKTLQLAVAINQEPPDAKMLQMVLOGSV

**Coiled-Coil 2**

HC2A	SVQVNAGPLAYARAFLDDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLDDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLDDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLNDSQASKYPPKKVSELKDMFRKFQACSTIAELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKRLCFKDFTKRCEDALRKNKSLIGPVQKE
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKRLCFKEFIMRCGEAVEKNKRLITADQRE

**Coiled-Coil 2**

HC2A	YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPTSTMVHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHEQLG-----
rat	YQEEMKANYREIRKELSDIIVERICPGEDKRATKFP AHLQRHQRTDNKHSGSRVDQFILS
HC4	YHEGLKSNFRDMVKELSDIIHEQILQEDTMHSPWMSNTLHVFC AISGTSSDRGYGSPRYA
HC1	YQEELRSHYKDMSELSTVMNEQITGRDDLSK---RGVDQTCTRVIISKATPALPTVSISS
HC3	YORELG---KLSS-----P-----
HC5	YQQELKKNNKLNKLENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS--

PBM

HC2A	SSVV-----
KIAA	-----
rat	CVTLPHEPHVGTCFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWCK
HC4	EV-----
HC1	SAEV-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	-----
rat	VHIFF
HC4	-----
HC1	-----
HC3	-----
HC5	-----
RNTVLTT	

**FIG. 4B (5 of 5)**

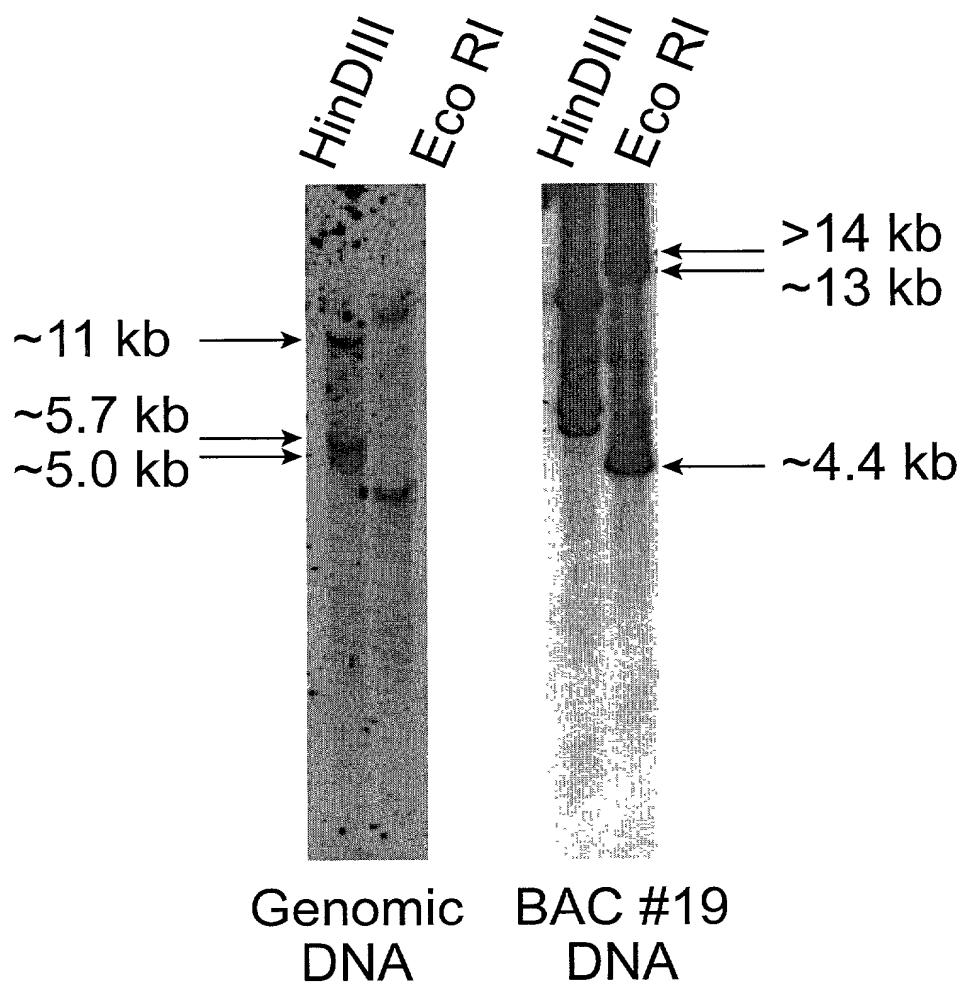


FIG. 5

-111

CGGTAACCGCCATTTGTCTCCTGTAACAATTACGCGCCGTGTAACGTGAATCTTCAAAGCCTCAGTTTATGACC  
CTGTGGAGCCAGTGGACTTTGAAGGACTTCTG -1

1/1

31/11

ATG ACA CAC CTG AAC AGC CTG GAT GTG CAG CTT GCC CAG GAG CTC GGG GAC TTC ACT GAT  
Met thr his leu asn ser leu asp val gln leu ala gln glu leu gly asp phe thr asp  
61/21 91/31

GAC GAC TTG GAC GTG GTG TTC ACG CCA AAG GAA TGT AGG ACT TTG CAG CCC TCT TTG CCG  
asp asp leu asp val val phe thr pro lys glu cys arg thr leu gln pro ser leu pro  
121/41 151/51

GAG GAA GGG GTT GAA CTG GAC CCT CAT GTC AGG GAC TGT GTT CAG ACC TAC ATC CGT GAG  
glu glu gly val glu leu asp pro his val arg asp cys val gln thr tyr ile arg glu  
181/61 211/71

TGG CTA ATC GTG AAC CGG AAA AAC CAA GGA AGT CCA GAA ATC TGT GGC TTT AAA AAG ACT  
trp leu ile val asn arg lys asn gln gly ser pro glu ile cys gly phe lys lys thr  
241/81 271/91

GGA TCT CGA AAA GAT TTT CAC AAG ACG CTT CCG AAA CAG ACG TTT GAG TCG GAA ACC TTG  
gly ser arg lys asp phe his lys thr leu pro lys gln thr phe glu ser glu thr leu  
301/101 331/111

GAG TGC AGT GAA CCC GCT GCT CAG GCA GGC CCC CGC CAC TTA AAC GTG CTG TGC GAC GTG  
glu cys ser glu pro ala ala gln ala gly pro arg his leu asn val leu cys asp val  
361/121 391/131

TCT GGG AAA GGC CCC GTC ACT GCC TGT GAC TTT GAC CTC CGC AGC CTG CAG CCT GAC AAG  
ser gly lys gly pro val thr ala cys asp phe asp leu arg ser leu gln pro asp lys  
421/141 451/151

CGG CTA GAA AAC CTC CTG CAG CAA GTG AGT GCC GAG GAC TTT GAG AAG CAG AAC GAG GAG  
arg leu glu asn leu leu gln gln val ser ala glu asp phe glu lys gln asn glu glu  
481/161 511/171

GCC CGG AGG ACC AAC AGG CAG GCC GAG CTC TTT GCC CTT TAC CCA TCA GTG GAC GAG GAG  
ala arg arg thr asn arg gln ala glu leu phe ala leu tyr pro ser val asp glu glu  
541/181 571/191

GAT GCT GTG GAA ATA CGT CCA GTA CCA GAA TGT CCC AAG GAA CAC CTG GGC AAC AGA ATA  
asp ala val glu ile arg pro val pro glu cys pro lys glu his leu gly asn arg ile  
601/201 631/211

TTG GTC AAG TTG CTG ACC TTG AAG TTC GAG ATT GAA ATT GAG CCC CTG TTT GCC AGC ATT  
leu val lys leu leu thr leu lys phe glu ile glu ile glu pro leu phe ala ser ile  
661/221 691/231

GCC CTC TAC GAT GTT AAA GAA AGG AAA AAG ATC TCA GAA AAT TTT CAC TGT GAC CTG AAC  
ala leu tyr asp val lys glu arg lys lys ile ser glu asn phe his cys asp leu asn  
721/241 751/251

TCT GAC CAG TTC AAA GGA TTT CTG CGA GCT CAC ACG CCT TCA GTG GCC GCA TCA AGT CAG  
ser asp gln phe lys gly phe leu arg ala his thr pro ser val ala ala ser ser gln  
781/261 811/271

GCG AGA TCT GCA GTC TTC TCA GTC ACC TAC CCG TCC TCA GAC ATC TAC CTG GTA GTC AAG  
ala arg ser ala val phe ser val thr tyr pro ser ser asp ile tyr leu val val lys  
841/281 871/291

ATT GAA AAA GTC CTG CAG CAG GGA GAT ATT GGA GAC TGT GCA GAG CCC TAC ACG GTT ATC  
ile glu lys val leu gln gln gly asp ile gly asp cys ala glu pro tyr thr val ile  
901/301 931/311

AAA GAA AGT GAT GGT GGA AAG AGT AAA GAA AAG ATT GAA AAA CTA AAA CTC CAA GCT GAA  
lys glu ser asp gly gly lys ser lys glu lys ile glu lys leu lys leu gln ala glu  
961/321 991/331

TCC TTC TGC CAG CGT TTG GGG AAA TAC CGG ATG CCC TTT GCC TGG GCA CCC ATA AGC TTA  
ser phe cys gln arg leu gly lys tyr arg met pro phe ala trp ala pro ile ser leu

1021/341 1051/351  
 TCA AGC TTC TTC AAT GTC TCC ACC CTT GAG AGG GAG GTA ACT GAT GTG GAC TCT GTG GTT  
 ser ser phe asn val ser thr leu glu arg glu val thr asp val asp ser val val  
 1081/361 1111/371  
 GGG AGA AGC CCA GTG GGT GAA CGG AGG ACA TTG GCC CAA TCT AGA AGG CTT TCT GAA AGA  
 gly arg ser pro val gly glu arg arg thr leu ala gln ser arg arg leu ser glu arg  
 1141/381 1171/391  
 GCC CTC TCC TTG GAG GAA AAT GGG GTT GGA TCC AAC TTC AAA ACC TCC ACT CTG AGC GTT  
 ala leu ser leu glu glu asn gly val gly ser asn phe lys thr ser thr leu ser val  
 1201/401 1231/411  
 AGC AGC TTT TTC AAG CAG GAA GGA GAT CGC CTT AGC GAT GAA GAC TTA TTC AAG TTT TTA  
 ser ser phe phe lys gln glu gly asp arg leu ser asp glu asp leu phe lys phe leu  
 1261/421 1291/431  
 GCT GAC TAC AAA AGA TCA TCA TCC TTA CAG AGA CGA GTC AAG TCA ATT CCA GGC TTG CTA  
 ala asp tyr lys arg ser ser ser leu gln arg arg val lys ser ile pro gly leu leu  
 1321/441 1351/451  
 AGA CTG GAG ATT TCT ACA GCT CCA GAG ATC ATC AAT TGC TGT CTG ACT CCT GAA ATG CTG  
 arg leu glu ile ser thr ala pro glu ile ile asn cys cys leu thr pro glu met leu  
 1381/461 1411/471  
 CCC GTG AAA CCC TTT CCT GAA AAC CGG ACA CGC CCG CAC AAA GAG ATT TTG GAA TTT CCA  
 pro val lys pro phe pro glu asn arg thr arg pro his lys glu ile leu glu phe pro  
 1441/481 1471/491  
 ACA CGA GAA GTA TAT GTC CCT CAC ACT GTG TAC AGA AAC CTT CTC TAT GTC TAC CCA CAG  
 thr arg glu val tyr val pro his thr val tyr arg asn leu leu tyr val tyr pro gln  
 1501/501 1531/511  
 AGG CTG AAC TTT GTA AAC AAA CTA GCA TCA GCC CGG AAC ATT ACA ATA AAG ATC CAG TTT  
 arg leu asn phe val asn lys leu ala ser ala arg asn ile thr ile lys ile gln phe  
 1561/521 1591/531  
 ATG TGT GGA GAA GAT GCT AGC AAT GCG ATG CCG GTC ATC TTT GGA AAA TCC AGC GGG CCT  
 met cys gly glu asp ala ser asn ala met pro val ile phe gly lys ser ser gly pro  
 1621/541 1651/551  
 GAA TTT CTG CAG GAA GTG TAC ACA GCT GTT ACA TAC CAT AAT AAG TCT CCT GAC TTT TAT  
 glu phe leu gln glu val tyr thr ala val thr tyr his asn lys ser pro asp phe tyr  
 1681/561 1711/571  
 GAA GAA GTG AAA ATT AAG CTC CCC GCT AAG CTC ACA GTA AAT CAC CAC CTC CTG TTC ACC  
 glu glu val lys ile lys leu pro ala lys leu thr val asn his his leu leu phe thr  
 1741/581 1771/591  
 TTC TAC CAT ATC AGC TGT CAG CAG AAG CAA GGA GCC TCC GTG GAA ACT CTC CTG GGA TAT  
 phe tyr his ile ser cys gln gln lys gln gly ala ser val glu thr leu leu gly tyr  
 1801/601 1831/611  
 TCA TGG CTG CCA ATT CTC TTA AAT GAA CGT CTT CAA ACT GGA TCC TAC TGT CTC CCA GTT  
 ser trp leu pro ile leu leu asn glu arg leu gln thr gly ser tyr cys leu pro val  
 1861/621 1891/631  
 GCC TTG GAA AAA TTG CCA CCC AAC TAC TCC ATG CAT TCT GCT GAG AAA GTC CCA TTA CAG  
 ala leu glu lys leu pro pro asn tyr ser met his ser ala glu lys val pro leu gln  
 1921/641 1951/651  
 AAT CCT CCC ATT AAG TGG GCT GAA GGA CAT AAG GGA GTA TTT AAT ATT GAA GTG CAA GCT  
 asn pro pro ile lys trp ala glu gly his lys gly val phe asn ile glu val gln ala  
 1981/661 2011/671  
 GTT TCT TCT GTA CAC ACC CAG GAC AAC CAC CTG GAG AAG TTC TTC ACC CTC TGC CAC TCC  
 val ser ser val his thr gln asp asn his leu glu lys phe phe thr leu cys his ser  
 2041/681 2071/691  
 CTG GAG AGC CAG GTG ACC TTC CCC ATC CGC GTG CTG GAT CAG AAA ATC AGC GAG ATG GCG  
 leu glu ser gln val thr phe pro ile arg val leu asp gln lys ile ser glu met ala  
 2101/701 2131/711  
 CTG GAG CAT GAG CTG AAG CTC AGC ATC ATC TGC CTG AAC TCC TCC CGC CTG GAG CCG CTC  
 leu glu his glu leu lys leu ser ile ile cys leu asn ser ser arg leu glu pro leu

FIG. 6A (2 of 6)

2161/721 2191/731  
 GTG CTC TTC CTG CAC CTG GTG CTG GAC AAG CTC TTC CAG CTG TCC GTG CAG CCC ATG GTC  
 val leu phe leu his leu val leu asp lys leu phe gln leu ser val gln pro met val  
 2221/741 2251/751  
 ATC GCT GGC CAG ACA GCC AAC TTC TCC CAG TTT GCC TTC GAG TCC GTG GTG GCC ATC GCC  
 ile ala gly gln thr ala asn phe ser gln phe ala phe glu ser val val ala ile ala  
 2281/761 2311/771  
 AAC AGT CTG CAC AAC AGC AAG GAC CTG AGC AAG GAC CAG CAT GGG AGG AAC TGC CTG CTG  
 asn ser leu his asn ser lys asp leu ser lys asp gln his gly arg asn cys leu leu  
 2341/781 2371/791  
 GCT TCC TAC GTG CAC TAC GTC TTC CGC CTG CCA GAG GTG CAA AGG GAT GTG CCC AAG TCA  
 ala ser tyr val his tyr val phe arg leu pro glu val gln arg asp val pro lys ser  
 2401/801 2431/811  
 GGC GCT CCC ACT GCC CTC CTA GAC CCT CGG AGC TAC CAC ACG TAT GGC CGC ACA TCA GCT  
 gly ala pro thr ala leu leu asp pro arg ser tyr his thr tyr gly arg thr ser ala  
 2461/821 2491/831  
 GCT GCT GTG AGT TCA AAG CTG CTG CAG GCC CGG GTG ATG AGC AGC AGT AAC CCA GAC CTC  
 ala ala val ser ser lys leu leu gln ala arg val met ser ser ser asn pro asp leu  
 2521/841 2551/851  
 GCG GGG ACA CAC TCC GCA GCA GAC GAG GAA GTG AAG AAC ATC ATG TCT TCA AAG ATC GCC  
 ala gly thr his ser ala ala asp glu glu val lys asn ile met ser ser lys ile ala  
 2581/861 2611/871  
 GAT CGC AAC TGC AGC CGA ATG TCT TAC TAT TGC TCT GGC AGT AGT GAT GCT CCA AGT TCA  
 asp arg asn cys ser arg met ser tyr tyr cys ser gly ser ser asp ala pro ser ser  
 2641/881 2671/891  
 CCT GCA GCC CCA AGG CCA GCC AGC AAA AAG CAT TTC CAT GAG GAG CTT GCC CTT CAG ATG  
 pro ala ala pro arg pro ala ser lys lys his phe his glu glu leu ala leu gln met  
 2701/901 2731/911  
 GTG GTC AGC ACC GGA ATG GTG AAA AGC ATG GCC CAG CAC GTA CAT AAC ATG GAC AAA CGG  
 val val ser thr gly met val lys ser met ala gln his val his asn met asp lys arg  
 2761/921 2791/931  
 GAC AGT TTT CGG AGG ACT CGT TTT TCT GAC CGT TTC ATG GAT GAC ATA ACT ACT ATT GTT  
 asp ser phe arg arg thr arg phe ser asp arg phe met asp asp ile thr thr ile val  
 2821/941 2851/951  
 AAT GTG GTC ACC TCG GAA ATT GCA GCC CTT TTA GTA AAA CCA CAG AAG GAA AAT GAA CAG  
 asn val val thr ser glu ile ala ala leu leu val lys pro gln lys glu asn glu gln  
 2881/961 2911/971  
 GCG GAA AAG ATG AAC ATC AGC CTG GCT TTC TTG TAT GAC CTT CTC TCC CTC ATG GAT  
 ala glu lys met asn ile ser leu ala phe phe leu tyr asp leu leu ser leu met asp  
 2941/981 2971/991  
 CGG GGC TTT GTG TTT AAC CTC ATC AGA CAT TAT TGC AGC CAG CTG TCA GCC AAG CTC AGT  
 arg gly phe val phe asn leu ile arg his tyr cys ser gln leu ser ala lys leu ser  
 3001/1001 3031/1011  
 AAC CTT CCA ACG CTC ATT TCC ATG AGG CTA GAG TTC CTG AGA ATC CTC TGT AGC CAT GAG  
 asn leu pro thr leu ile ser met arg leu glu phe leu arg ile leu cys ser his glu  
 3061/1021 3091/1031  
 CAT TAC CTC AAT CTG AAC CTT TTT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT  
 his tyr leu asn leu asn leu phe phe met asn ala asp thr ala pro thr ser pro cys  
 3121/1041 3151/1051  
 CCT TCC ATA TCT TCC CAG AAC TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC  
 pro ser ile ser ser gln asn ser ser ser cys ser ser phe gln asp gln lys ile ala  
 3181/1061 3211/1071  
 AGC ATG TTC GAT CTG ACT TCC GAG TAC CGC CAG CAG CAC TTC CTC ACC GGG CTC CTC TTC  
 ser met phe asp leu thr ser glu tyr arg gln gln his phe leu thr gly leu leu phe  
 3241/1081 3271/1091  
 ACA GAA CTG GCT GCT GCC CTG GAT GCC GAA GGG GAA GGA ATC AGC AAA GTA CAA AGG AAA  
 thr glu leu ala ala ala leu asp ala glu gly glu gly ile ser lys val gln arg lys

FIG. 6A (3 of 6)

3301/1101 3331/1111  
 GCT GTC AGT GCA ATT CAC AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA  
 ala val ser ala ile his ser leu leu ser ser his asp leu asp pro arg cys val lys  
 3361/1121 3391/1131  
 CCA GAG GTG AAG GTC AAA ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT  
 pro glu val lys val lys ile ala ala leu tyr leu pro leu val gly ile ile leu asp  
 3421/1141 3451/1151  
 GCT TTG CCA CAG CTC TGT GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC  
 ala leu pro gln leu cys asp phe thr val ala asp thr arg arg tyr arg thr ser gly  
 3481/1161 3511/1171  
 TCG GAT GAA GAA CAA GAA GGA GCC GGT GCC ATT AAC CAG AAT GTG GCT CTG GCC ATA GCA  
 ser asp glu glu gln glu gly ala gly ala ile asn gln asn val ala leu ala ile ala  
 3541/1181 3571/1191  
 GGG AAT AAT TTC AAT TTG AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG  
 gly asn asn phe asn leu lys thr ser gly ile val leu ser ser leu pro tyr lys gln  
 3601/1201 3631/1211  
 TAC AAC ATG CTG AAC GCG GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG  
 tyr asn met leu asn ala asp thr thr arg asn leu met ile cys phe leu trp ile met  
 3661/1221 3691/1231  
 AAA AAT GCT GAT CAG AGC CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC  
 lys asn ala asp gln ser leu ile arg lys trp ile ala asp leu pro ser thr gln leu  
 3721/1241 3751/1251  
 AAC AGG ATT TTA GAT CTA CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG  
 asn arg ile leu asp leu leu phe ile cys val leu cys phe glu tyr lys gly lys gln  
 3781/1261 3811/1271  
 AGT TCT GAC AAA GTC AGT ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG  
 ser ser asp lys val ser thr gln val leu gln lys ser arg asp val lys ala arg leu  
 3841/1281 3871/1291  
 GAA GAG GCT TTG CTG CGT GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA  
 glu glu ala leu leu arg gly glu gly ala arg gly glu met met arg arg arg ala pro  
 3901/1301 3931/1311  
 GGG AAC GAC CGA TTT CCA GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT  
 gly asn asp arg phe pro gly leu asn glu asn leu arg trp lys lys glu gln thr his  
 3961/1321 3991/1331  
 TGG CGG CAA GCT AAT GAG AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG  
 trp arg gln ala asn glu lys leu asp lys thr lys ala glu leu asp gln glu ala leu  
 4021/1341 4051/1351  
 ATC AGT GGC AAT CTG GCT ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT  
 ile ser gly asn leu ala thr glu ala his leu ile ile leu asp met gln glu asn ile  
 4081/1361 4111/1371  
 ATC CAG GCG AGC TCG GCT CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG  
 ile gln ala ser ser ala leu asp cys lys asp ser leu leu gly gly val leu arg val  
 4141/1381 4171/1391  
 CTG GTG AAT TCT CTG AAC TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA  
 leu val asn ser leu asn cys asp gln ser thr thr tyr leu thr his cys phe ala thr  
 4201/1401 4231/1411  
 CTC CGT GCT CTC ATC GCC AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT  
 leu arg ala leu ile ala lys phe gly asp leu leu phe glu glu glu val glu gln cys  
 4261/1421 4291/1431  
 TTC GAC CTA TGT CAC CAA GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC  
 phe asp leu cys his gln val leu his his cys ser ser ser met asp val thr arg ser  
 4321/1441 4351/1451  
 CAA GCC TGT GCC ACC CTT TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT  
 gln ala cys ala thr leu tyr leu leu met arg phe ser phe gly ala thr ser asn phe  
 4381/1461 4411/1471  
 GCA AGA GTA AAG ATG CAA GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC  
 ala arg val lys met gln val thr met ser leu ala ser leu val gly arg ala pro asp

4441/1481

TTT AAT GAA GAG CAC CTG AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC  
phe asn glu glu his leu arg arg ser leu arg thr ile leu ala tyr ser glu glu asp  
4501/1501 4531/1511

ACA GCC ATG CAG ATG ACT CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT  
thr ala met gln met thr pro phe pro thr gln val glu glu leu leu cys asn leu asn  
4561/1521 4591/1531

AGC ATC TTA TAT GAC ACA GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG  
ser ile leu tyr asp thr val lys met arg glu phe gln glu asp pro glu met leu met  
4621/1541 4651/1551

GAT CTC ATG TAC AGA ATT GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG  
asp leu met tyr arg ile ala lys ser tyr gln ala ser pro asp leu arg leu thr trp  
4681/1561 4711/1571

CTC CAG AAC ATG GCA GAG AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC  
leu gln asn met ala glu lys his thr lys lys cys tyr thr glu ala ala met cys  
4741/1581 4771/1591

CTG GTG CAC GCC GCT GCG TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC  
leu val his ala ala ala leu val ala glu tyr leu ser met leu glu asp his ser tyr  
4801/1601 4831/1611

CTG CCC GTG GGC AGT GTC AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG  
leu pro val gly ser val ser phe gln asn ile ser ser asn val leu glu glu ser val  
4861/1621 4891/1631

GTC TCT GAG GAC ACC CTG TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC  
val ser glu asp thr leu ser pro asp glu asp gly val cys ala gly gln tyr phe thr  
4921/1641 4951/1651

GAG AGT GGC CTG GTA GGC CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA  
glu ser gly leu val gly leu leu glu gln ala ala glu leu phe ser thr gly gly leu  
4981/1661 5011/1671

TAT GAG ACA GTT AAT GAG GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA  
tyr glu thr val asn glu val tyr lys leu val ile pro ile leu glu ala his arg glu  
5041/1681 5071/1691

TTC CGG AAG CTG ACA CTC ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC  
phe arg lys leu thr leu thr his ser lys leu gln arg ala phe asp ser ile val asn  
5101/1701 5131/1711

AAG GAT CAT AAG AGA ATG TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT  
lys asp his lys arg met phe gly thr tyr phe arg val gly phe phe gly ser lys phe  
5161/1721 5191/1731

GGG GAT TTG GAT GAA CAG GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG  
gly asp leu asp glu gln glu phe val tyr lys glu pro ala ile thr lys leu pro glu  
5221/1741 5251/1751

ATC TCA CAT AGA CTA GAG GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG  
ile ser his arg leu glu ala phe tyr gly gln cys phe gly ala glu phe val glu val  
5281/1761 5311/1771

ATT AAA GAC TCC ACT CCT GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG  
ile lys asp ser thr pro val asp lys thr lys leu asp pro asn lys ala tyr ile gln  
5341/1781 5371/1791

ATC ACT TTT GTG GAG CCC TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT  
ile thr phe val glu pro tyr phe asp glu tyr glu met lys asp arg val thr tyr phe  
5401/1801 5431/1811

GAG AAG AAT TTC AAC CTC CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG  
glu lys asn phe asn leu arg arg phe met tyr thr thr pro phe thr leu glu gly arg  
5461/1821 5491/1831

CCT CGG GGA GAG CTG CAT GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC  
pro arg gly glu leu his glu gln tyr arg arg asn thr val leu thr thr met his ala  
5521/1841 5551/1851

TTC CCC TAC ATC AAG ACC AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG  
phe pro tyr ile lys thr arg ile ser val ile gln lys glu glu phe val leu thr pro

5581/1861

ATT GAA GTT GCC ATT GAA GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC  
ile glu val ala ile glu asp met lys lys lys thr leu gln leu ala val ala ile asn  
5641/1881

5671/1891

CAG GAG CCG CCT GAT GCA AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT  
gln glu pro pro asp ala lys met leu gln met val leu gln gly ser val gly ala thr  
5701/1901

5731/1911

GTA AAT CAG GGA CCA CTG GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA  
val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro ala asp pro  
5761/1921

5791/1931

AAA CTC TAT CGA CAT CAC AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT  
lys leu tyr arg his his asn lys leu arg leu cys phe lys glu phe ile met arg cys  
5821/1941

5851/1951

GGT GAA GCT GTA GAG AAA AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG  
gly glu ala val glu lys asn lys arg leu ile thr ala asp gln arg glu tyr gln gln  
5881/1961

5911/1971

GAA CTC AAA AAG AAC TAT AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA  
glu leu lys lys asn tyr asn lys leu lys glu asn leu arg pro met ile glu arg lys  
5941/1981

5971/1991

ATT CCA GAA CTG TAC AAG CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC  
ile pro glu leu tyr lys pro ile phe arg val glu ser gln lys arg asp ser phe his  
6001/2001

6031/2011

AGA TCT AGT TTC AGG AAA TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA  
arg ser ser phe arg lys cys glu thr gln leu ser gln gly ser OCH

GAAAAGCCATCTTCATTCGTGGAGACTGTGGCCCTGCAACCCCTGGAGAAGGACTTGTGGTACTTAAAAAAATGGGACATT  
TGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCCTCTGGAGCTTGGGATCCCAGGAACCATGGAATTATT  
CCCAAATGGACTCTGACCAGATTGGCATACTGGGGGGTGGGGATGGAGGATGGGTACTCAGGCATGACTGCGTAT  
TTATTAAGTGTGTTTCCACATGTACCAACAAGGCATAAGCAGCTCTCTGCTGACTGGCCAATCAGCCAT  
TGAGAGATGATTCCTCTGGCCCATATTGAATTTATTGGAGTAACTCAAATTGCTGAGGAAAAATGGAAAAATTATCC  
ACCAGTCGATTCAAACGTGAATTCACTCTTATAGGAAGGCAGGGCAAACCTGTAGGAGTACGAAACATTTCATAAAAT  
CTACAAAGGGAGCCTTACTACAATTCCAAAATCATCATGGTTGAAATTGGGAGGAGATTATTGTGAACCTGTTAC  
CCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTATTGGTTATTACTGTTACATTAATTAAACATGCATT  
TAGAAGAATAACATTCAAAGCACTGATGTAGGAGATAACAGGTACTTGGAGCAGTCAGCCAAAATCACAGATACTGCTT  
CACTTAAATGGAAACAATTCTCCGATAATGCTTGTCTTTCTTATGTCACTCTGTGTACTATCTATTTCCTCCT  
TCTGGGACCAAGTTCTTTTATAAAGCAATAATCTCTGTCTTCAGAACATTGTGCTGTGTAGCATATGT  
ATATCAGCTACAAAATATATTCAACTTTGACTCTTTGACAAAGGACTTAGGAAAAGGAGGAACAAAGACATTATTG  
AGAATTAATTATATTTAATATGACTGTGACCTTGACTGATAATAAGATGTAATAAGAATTGCAAGCTAAAAAA  
AAAAAAAAAAACTCG

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-5 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1727	C to T change; mis-sense mutation changing codon from alanine to valine
2	1749	A to G change; silent mutation
3	2277	G to C change; silent mutation
4	2853	C to T change; silent mutation
5	3427	A to G change; mis-sense mutation changing codon from lysine to glutamic acid
6	3777	C to T change; silent mutation

B. Alternative splices

Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	1806-1944	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein
2	exon insertion	between 2857 and 2858	additional, in-frame 48 nucleotide exon that contains a stop codon at the second codon, which would lead to a truncated, most likely soluble protein

These differences may be found separately or together in various combinations in the different human CLASP-5 isoforms

FIG. 6B

552 nt overlap

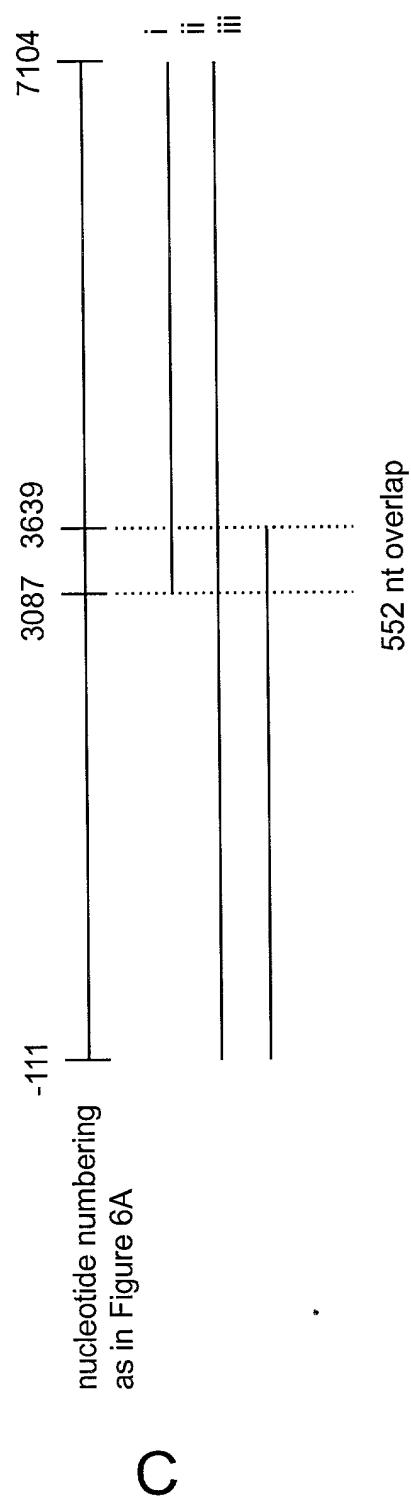


FIG. 6C

1st partial exon (nucleotides 3793 to 3952)

CCAGCTGTCAGCCAAGCTCAGTAACCTCCAACGCTCATTTCCATGAGGCTAG  
AGTTCCCTGAGAATCCTCTGTAGCCATGAGCATTACCTCAATCTGAACCTTTT  
TTATGAATGCTGATACTGCTCCAACATCTCCTGTCCTCCATATCTCCCAG  
GTAATAAAAGAATTATTAACAAAAGAATTATTCAAGCTAT

2nd exon (nucleotides 5809 to 5948)

GCTCATAAAATGGCTCCTTACGTTCTGTAGAACTCAAGCTCCTGCTCCAGCT  
TCCAGGACCAGAAGATCGCCAGCATGTTCGATCTGACTTCCGAGTACCGCCA  
GCAGCACTTCCTCACCGGGCTCCTCTCACAGAACTGGCTGCTGCCCTGGATG  
CCGAAGGGGAAGGGTATGTTCTGGCATTAAAATGGAAGATGAAGC

3rd exon (nucleotides 13662 to 13831)

CATAACCTCTGATTCTGTGTTGTGCCAACAGAACATCAGCAAAGTACAAAGG  
AAAGCTGTCAGTGCAATTACAGCCTGCTAACAGTCTCACGACCTGGACCCAC  
GCTGTGTCAAACCAGAGGTGAAGGTAAAATGCCGCCCTTACCTACCTTTA  
GTGGCATTTCGGATGCTTGCACAGCTCTGTGACTTACAGGTAATGG  
CCCTCTGTTCTTGGATTG

4th exon (nucleotides 16948 to 17087)

TGTTTGACTTGACATCACAAACGATGTTTCATTGCAGTTGCAGATACTCGCA  
GATACCGCACCAGTGGCTCGGATGAAGAACAAAGAAGGAGCCGGTGCCATTA  
ACCAGAAATGTGGCTCTGCCATAGCAGGAAATAATTCAATTGAAAACAAG  
TGGAATAGTGTGCTTCCCTGGATGTTGGTGCACATGTGTCTGGTGATTT  
TCAT

5th exon (nucleotides 19281 to 19463)

TGGCCTCCATCCCCAATCTGCCTCCCTCAGCCCTATAAGCAGTACAACATG  
CTGAACCGGGACACTACTCGCAACCTCATGATCTGCTTCCTCTGGATCATGAA  
AAATGCTGATCAGAGCCTCATTAGGAAGTGGATTGCTGACCTGCCATCAACG  
CAGCTCAACAGGATTTAGATCTACTTTCATCTGTGTGTTATGTTGAGTAT  
AAGGTAAGTCTGGAGTGGCACAACTTATACCAAGC

6th exon (nucleotides 19829 to 19958)

CACCAAAGGACATGTCCTCCTACCTCTGTCTGTCAGGGAAAACAGAGTTCT  
GACAAAGTCAGTACCCAAAGTCCTGCAAGTCAAGGGATGTCAAGGCCGG  
CTGGAAAGAGGCTTGCTGCGTGGGAAGGGGCCAGAGGGGAGATGATGCGC  
CGCCGGGCTCCAGGTGTGGACTGCCCTCCCTGCTCTGTCAAGC

7th exon (nucleotides 20928 to 21015)

TCAAATTCTATCATGCATTCTTAACCTCTAGGGAACGACCGATTCAGGC  
CTAAATGAAAATTGAGATGGAAGAAAGAGCAGACACATTGGCGGCAAGCT  
AATGAGAAGCTAGATAAGTGAGTCACTCGGCAACTTCTGCTACTTTACCT

8th exon (nucleotides 25765 to 25861)

GCTTAATTGACCTCTTGTGTTCTAGAACAAAGGCCGAGTTAGATCAAG  
AAGCCTTGATCAGTGGCAATCTGGCTACAGAAGCACATTAAATCATCCTGGA  
TATGCAGGAAAACATTATCCAGGTGAGGAAACAAACACCCAACTTGATTG

9th exon (nucleotides 27242 to 27376)

GGATTCAATGATGCTGTTCTCCATTCCCCCAGGCGAGCTCGGCTCTGGACTG  
TAAAGACAGCCTGCTGGGAGGTGTTCTGAGGGTGCTGGTAATTCTCTGAAC  
TGTGATCAGAGTACCACTACCTGACTCACTGCTTGCAACACTCCGTGCTCT  
CATGCCAAGGTAACGGATGCTTGTGTTCTCCCTTAATT

10th exon (nucleotides 28582 to 28734)

AGTGATGCCAATGCCCTTATGTCTCTCTAGTTGGAGACTTACTCTTCG  
AAGAGGAGGTGGAACAGTGTTGACCTATGTCAACCAAGTCCTGCACCACTG  
CAGCAGCAGCATGGATGTCAACCGGAGCCAAGCCTGTGCCACCCCTTACCTC  
CTCATGAGGTTCACTTGGAGCCACCAAGTGTAAAGAGTTCAAACCAGCTGAG  
TGACCTGGAATCAG

11th exon (nucleotides 31046 to 31204)

TTACTTCATCTTTTTTTTTTCACTGATGCAGAATTGCAAGAGTAAAGA  
TGCAAGTAACCATGTCCTGGCATCTTGGTGGAAAGAGCACCAGACTTTAA  
TGAAGAGCACCTGAGAAGATCCTTGAGGACAATTGGCCTATTAGAAGAG  
GACACAGCCATGCAGATGACTCCTTCCCACCCAGGTACACCGAACAT  
ACCTTGTCTCATGCATGAGT

12th exon (nucleotides 32755 to 32855)

AGCTAAGATTATTTGAGGCTTACACTTTGCAGGTGGAGGAACCTCTCTGT  
AATCTGAATAGCATCTTATATGACACAGTGAAAATGAGGGAAATTCAAGGAAG  
ATCCTGAGATGCTTATGGATCTCATGTACAGGTAAAGCTTCTGACACACTCA  
AGGGACACCATT

13th exon (nucleotides 33663 to 33855)

TCCTCAAAACTACTCTCACTCAATCTGTCTCAGAATTGCCAAGAGTTACCA  
GGCATCTCCTGATCTGGCTGACCTGGCTCCAGAACATGGCAGAGAACACAC  
CAAGAAGAAGTGCACACGGAGGCTGCCATGTGCCTGGTGCACGCCGCTG  
CGTTAGTGGCTGAGTATCTGAGCATGCTGGAGGACACAGCTACCTGCCGT  
GGGCAGTGTCAAGCTTCCAGGTAGGGTGTGCAAGCTTCCCTAGAGCAGTG  
GTTC

FIG. 7A (2 of 4)

14th exon (nucleotides 38125 to 38268)

CTGTTCTCCAGGCTTATACTGTGGTCTCTTCAGAATTTCTCCAATGTGCT  
GGAGGAGTCTGTGGTCTCTGAGGACACCCTGTCACCTGACGAGGATGGGGTGTG  
CGCAGGCCAGTACTTCACCGAGAGTGGCCTGGTAGGCCTCCTGGAGCAGG  
CCGCGGGAGCTTTCAGCACGGTCAGTGCCCCAGAGGCATCCCGGGGCTGGC  
C

15th exon (nucleotides 40166 to 40297)

AATTCTCTGTATGCTCTCCCTTTCCAAAGGGAGGCTTATGAGACAGT  
TAATGAGGCTTACAAAGCTGGCTATCCCCATCCTAGAAAGCGCATCGAGAATTC  
CGGAAGCTGACACACTCACTACAGCAAGCTGCAGAGAGCCTCGACAGCGCATCG  
TTAAACAAGGTAGCCGGGGAGCCTGGCTGGCAGGCTTTGTTAC

16th exon (nucleotides 40755 to 40889)

TAAGGAGAGCTTTATTTGTTCCTCAGGATCTAAGAGAATGGTTGGAA  
CCTACTTCCGAGTTGGTTCTTTGGATCCAAATTTGGGGATTTGGATGAACAG  
GAGTTGTCTACAAAGAGCCTGCCAATACCAAGCTCCCTGGAGATCTCACAAG  
ACTAGAGGTAAAGAAAGTGTATCTGTGCGCCTGCACCTGGTACACTTTAC

17th exon (nucleotides 42307 to 42396)

AACCTTTATAAACTGTGGTTCTCTACCTAGGCATTTATGGTCAAGTTT  
GGTCAGAATTTGTGGAAGTGAATGAAAAGACTCCCACCTGTGGACAAACCA  
AGTTGGATCCTAACAAAGGTATACAAAAATTTACAAAAACTAACCAAGGC

18th exon (nucleotides 45250 to 45486)

TCTTCCCCTCCGTGCCTTTCCCCCTAGGCCTACATACAGATCACTTTGT  
GAGCCCTACTTGTATGAGTATGAAGATGAAAAGACAGGGTCACATCTGTGAGAAG  
ATTTCAACCTCCGGAGGTTCATGTACACCCACCCGTTCACCCCTGGAGGG  
GCGGCTCGGGAGAGGTGCATGAGCAGTCAGGAAGGAACACAGTCCTGTAC  
CACTATGCACGCCTCCCCCTACATCAAGACCCAGGATCAGCGGTCACCAGAA  
GAGGGAGGTAAATGCACCCAAAGGGATGGCCACCACTGGATGAGT

19th exon (nucleotides 48664 to 48807)

ACAGTGACTCCCTATGTTTACGTCTCAGTTCAGTTGTTTGACACCGATTG  
AAGTTGCCCATGAAGACATGAAGAGAAAGACCCCTGTCAGTTTAGCAGTTTGCCCAT  
TAACCCAGGGAGCCGCCTGTGACAAGATGTCTCAGTGGGTGCTAAGGGCTCTGT  
GGGAAGCTATGTAAATCAGGTAAGCAAAACCAAGAGGTGGGCAGCTCC

20th exon (nucleotides 50892 to 50998)

TATATTTTTTTTTTTTTTTTTTTCCACCAGGACCACTGGAAGTAGTC  
CCAAGTGTTTTTGGCTGAAAATCCCTGTGATCAAACCTATCGACATCACAAC  
AGTTGAGGTTTATGTCTTAAGGAATTCATCAGTGAGGTAAGAAAGGGAAATG  
GCTGGGAATTCAGTAGT

21st exon (nucleotides 62398 to 62568)

TCATTTATTCTCCCACACTGATATTTCATCTCAGATGTGGTGAAGCTGTAG  
AGAAAAACAAGCGTCTCATCACGGCAGACCAGAGGAAATATCAGCAGGAAC  
TCAAAAAGAACTATAACAAGCTAAAAGAGAACCTCAGGCCAATGATCGAGC  
GGAAAATTCCAGAACTGTACAAGCCAATATTAGAGTTGAGAGTCAAAAGAG  
GTAAGAACAGGGCAGAGGAGGCCTTCTGTGGGAT

22nd exon (nucleotides 63040 to 63294)

CCTCCCTCTTTCTTAATTTCAGGGACTCCTCACAGATCTAGTTCAGGA  
AATGTGAAACCCAGTTGTACAGGGCAGCTAAGAAAAGCCATCTCATTCTG  
GGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAAT  
GGGACATTGCCACCCAGGACTGACTGTACACTCCCTGATGCCAGCACTC  
TGGAGCTTGGGATCCCAGGAACCATGGAATTATTCCAAATGGACTCTGA  
CCAGATTTCGCCATACTGGGGGTGGCGGGATGGAGGATGGGTACTCAGGC  
ATGACTGCGTATTATTAAAGTGTGTTTCCACAATGTACCAAACAAGGCAT  
AAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCATCTGAGAGATGATT  
CTCTGGCCATATTGAATTATTGGAGTAACTCAAATTGCCTGAGGAAAAAT  
GGAAAAATTATCCACCAGTCGATTCAAACGTGAATTCACTCTTATAGGAAG  
GCAGGGCAAACTTGTTAGGAGTACGAAACATTCAATAATCTACAAAGGGA  
AGCCTTACTACAATTCCAAAATCATCATGGTTGGAAATTGGGAGGAGATT  
ATTGTGAACCTGTTACCCCTTGGTAATGGTGGACTAATTGCTGTATAGTTAT  
TTTGTGTTATTATTACTGTTACATTAATTAAACATGCATTATAGAAGAATAC  
ATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAA  
ATCACAGATACTGCTTCACTTAAATGAAACAATTCTCCGATAATGCTTGC  
TTTTTCTTATGTCACTCTGTGACTATCTATTTCCTCTGGGACCAA  
GTTTCTTTATAAAGCAATAATATCTGTTTCATTCAAGAACATTGTGCTG  
TCTGTCAGCATATGTATATCAGCTACAAATATTCAACTTGACTCTTTG  
ACAAAGGACTTTAGGAAAGGAGAACAAAGACATTATTGAGAATTAAATT  
ATATATTAAATATGACTGTGACCTTGACTGATAATAAGATGTAATAAGAA  
TTGCAAGCTAAAAAAAAAAAAAA

FIG. 7A (4 of 4)

GTTCTCTGGTTAGTCACTTAGTGACTTTAGATAAGTTTCCAATTTCAGGGCTTAATTCTCAGTTAAAATA  
 AGAAGGGGGGGTTGAGACATTGAGGGCTGATCAACGAAAAGGATAGGACCATAAAAAGCAGTGACATACAAGCTTCATT  
 GAGCAGCACTGGACACAGGGTACATAAGAGCGGAAGGCCCTCCAGCATGAGAACGCCATAGGCCCTGCAGTGAGGAGGG  
 GACCACATCCAGAGGACCAAGGGAACTCCCAGGGAGAGGAGGATTAGGGCAGAAGCTTATAGATCTGGGTGAGGCTGCTCC  
 ACAGCACAGTAGGGAGTCTGGGTAGAGAGCTCAAGGGCTGTAGCAGCTTAGGGCCCTGTATCTGCAAGGCTCTATC  
 TTATCATTAGGAAACAGCTGCCATCGAGATTATGGGTCTGCAAAGGAGGCACTAAATGGATGAAAATCTGCT  
 TATATGAGCTATTGGTAAATGACTGGCATGGTAAATTGAGTTAGGTATGAGCAAGGGATCAGCACCGATCGACA  
 GTGAAGAAAATAACAAACAGGAGGGCCAATACACAGAAACATCTTGACTTACATAACACCTCTCCAAAAAAA  
 GAAAAGACATGACTTTCTAAAGGAAGTCTGTACAGCCATACCAACCCCTGAACGCACGCACTCATCTAAGGAAAG  
 TCCGTAAAGGAAGCAGAATAATAAAAAGAATCTAAGGAAACATCAGAAGTCCCAAGCATCCCCATCCATGCACCC  
 TGACCCCTGCCCTGAGCGGATCTCTGTCCAGGACCCACAGAATAGAATGGCAGAGGGACACTTCACCTCTCTTG  
 CCTCCCTTCAGTATTAGGATTCAGGTAGTCTGTTCAAACCTTAAGTTAGTGTATGAAAGATAACCTAGATC  
 ACCACTGAGACCCAGGCTTAGCTACTCACATGCACTGAGGCTATCTCATCCGACAGGGAAATAAGCAACCCAAAGGCTA  
 TATCTGCTTCCCTGCAAACACTCATGTTTTATTCTCTCTTCTTCTCTTCTCTGCTCACTATCTTCTCC  
 TTAAATTCTCCCTTTCTTTAGTTACCATTTCTTTGTTCTCCTGACTCAAATGCCAAAGATCCCTAGACC  
 AGGAGTCAGAAGCCTGCATGCTATTCTGGACACCATTAACTACTCTGTGATTGGGAGCATCAGCCTTGAGGCAT  
 TCATTTCCATCTGCAAAAAAAACTAGGCTGATTAGATTATCCACTGATTCTGTGGTCTGTGCTGCCAGTGACATCC  
 ACGGATGTTACTTAGCACCATTAGTGGCACTCAGGCTCAGAAGGTCACTGACCCCCATTGTTGTTGATTAAATTCTG  
 ATCCCAGCTCTAGATAACAGGATGAACTTCACCTTAAGCAAGTTGATCTTACAAAGCTGCTGACTTTATCATT  
 TGCATAACCTATTATGTTTCTGCCATCTAAAGATTGGCAATGGATATAACCTTAGTCTTTTAATAGTCACAA  
 AAATAGACAAATCCATTCTCAATTACTGTCGACTTACAATGTCACCTACTCCTCTTCAACACCCATCCCTGGTAGGG  
 GCATTGTTGGCTTGGACCTTGGGAAGGGAAAGTTTGGATGACCTTACTCCTCTTCAACACCCATCCCTGGTAGGG  
 TTTGAAATGTCATTCTTTCTTGAGATGGAGCTTACTCTGTGCCCCAGGCCAGAGTGCAGTGGCACAATTGGC  
 TCACTGCAAAACTCCGCCCTCACAGGTTCAAGCGATTCTCCTCCTCACCCCTCCGAGTAGCTGGATTACAGGTGTGGC  
 ACCACTCCCCGCTAATTGGCATTAGAGACAGGGTTCACCATGTTGCCAGACTGGTCTGACTCTGGCCT  
 CAAGTGATCTGCCCTGCCCTGCCCTGGGAAGGTGCTGGGATTACAGGTGTGAGCCACCACACCCAGCCTGAAATGTC  
 TTGAATGATGTCCTAAGGGACCTATGAAAGATAACCCATAGTGGGCCCTTTAAGTGCCTGTTGTTGTTGAA  
 TTCCGATAGCCGGCTGACCCGACACCTGTTAATGAGTAACCTAAGTGACAGGCACATGACCAAGTTCTAACTCCCTCAA  
 TGTGCTGGTGGCTCACTGGTCAAAGTCAGCCAGGAGTGCACATGCAAAGGTTATGGGATCTGTTAATGCTTACAT  
 AGAAGTCATATGTTGGTTAAAATAATATAATGTCATTTACTTAAAGTGGATGTCATACTGAAATTAAATT  
 CTGAGGCAATATGTCCTCACACATTGGCTTCTGTTAAGGCTGAAATATGTTCAATTAAATTATGTT  
 GTCTGTAATCCCAGCACTTGGGAGGCCAAGGGGGAGGATCACCTGAGGCCAGGAGTTCGAGCAGCTGGCAATAT  
 GTTAAACCCCATCTACTAAAAAATACAAAAAATTAGCTGGCATGTTGATGTCACCTGTAATCCCAGCTACTCGGG  
 GGCTGAGGCAAGAGAATGCTGAAACCTGGGAGATGAAGGTTGCACTGAGGCCAGATCATGCCACTGCACTCCAGTTCAA  
 CAGAGCAAGACTCTGATCT  
 ATATATATGTTATATATGTTATATATGTTATATATGTTATATATGTTATATATGTTATATATGTTATATAT  
 ATATATATGTTAAAAAAACAAACTACTCTGAGTGAGTGAAAGAGGAGGAGCATGTCATACTACAAGGATGATGCTTCA  
 ATTTCTGCTGGGGGGGGGGGGGATGAAATGTCAGGAGGAGCATGTCAGGTCATCAGGCCCTTCCCTCCCT  
 TTGCTTCTAGAGGAGCTGCCCTGAGCTGGGTTCTCAGTTGTTCACTGCTGGGGAGCAAGGGCTCTTCA  
 GACAGTCACCTTCT  
 GCTTCT  
 TTGCTAAACAGTTGATGCTTCTCTAGGAACTGGTCTACAACCTTCAATGGGCCCTTAATTAGAAACTACGAG  
 AGAACACTGAGTATAAAAGTCATCTAGTCAATTCTATTAGTTCACTACAGGCTCATATGAGGTCACCTCAAGATT  
 TAGTTCTCGAACATAGTAGAGTTGTTGAAATTATGTTACGGTGAAGATGTACCTCAAGATTTCAGCACAGGC  
 TTCCCAGGTTAAAGGATAAGGAAATCGGATAAGAACATCTCATTCTGGACAGCTACTAGGCTAGAATCAC  
 TAAGGGAAACAGTAATGAAATGAAAATTATTAGACCTCTGTAATGCAAAATTACCATGTTGCACTATCCCATTAG  
 TTTTATTAATTGATTGCTTCAACCTGGAGAGAAAGGATATTGTTGTCAGGCCACCTCAACTCCACTACCTTGAA  
 TAAATGTTATTCCCTTTCT  
 GCTAGAGTCTGAGAATCTCTGAGCCATGAGCATTACCTCACTGTAACCTTGTGTTGTTGTTGTTGTTGTT  
 CAACATCTCTCTGCTCTCCATATCTCCAGGTAATAAGAATTATTAACCTAAAGAATTATTCAAGCTATTTCATT  
 TAACTAGCTAGTTAATCATGTTATCTCTATAAACGCTGTTCTTATTAATTGCAAAAGGAAATTCAAAACATTCAA  
 ATCAAGTATGCTACCTCTGAAAGTTACACCACTAGCTAAGAATTACATCTAAGTAAATTGTTCTCCCCAGGCTCAAGGC  
 TCCCTGATCAGGTTAAGTAAAGCCAAGAACATCCAATAAGGCCCTGAAATTGAAATTCTCAAGGAACTCTCAA  
 CTTGCTGACATTAGCCAATTGTTATATTGCAAAATGAGGATTCCAAAGTAAAGTAAATTGAAACCATGTTCA  
 CCAGGTTCTTGCACTGAGCAGGCCCTCAAGGAGTTTAACCTGTTCACTGTCATTGCAATGCAAGGAGCAAGGAG  
 AATGGGAGGAGGTGTCATGATAAGCAGTGAATTCCAAATGATTAAACATGAAACCCACCCACCTCATACATT  
 TGAAATGTTACTCTGAAATACTTAAGAACATGCTGTTGATAGTCACATTCAATTATAGGAAACACATCAGTAGCTC

FIG. 7B (1 of 15)

AGAGCATCAGGCAAATTCTCATTATTAGGTTATTCGTGCATATCCCTGATACTAGTACAAAAGTGAAGGCTT  
GTCTTACTAATTGAAAAAAATCTTAGCCATATATGCCATATGGCATGATCCAGATATTAGCTACATGACCACCTTACT  
GTGAACAGGGAAAGATCTGACTCACAAGCAGCAATTCAAATGATAAAACTTTGCTCCATCCTGCCAGCAGCTTAAG  
TCCTAAACCTCCCTGGACTAAGCTTACCCAGGTTCTTCCACCTTCCCTCTGACTGCCAGGGAGTGGCCAAAC  
CCAGGGGCCAGGCTCACAAAACCATGAAGGATTCTAAAGACACTTAGATGCTCTTAATGAAATATAAAGTGTGCTCC  
AGGATACAAATACAGGACAGGAATTACTGAGGACGGTAATCTATACTTCCCTCCCTGACATCACTTGTAGTTCCAGG  
CCAGCAAAAGTCTGACAATGTGCTTAAGCAAATTAGAAGTGTAGCTGAGGCCGGCACGGTGGCTCACATTGTAATC  
CCAGCATCTCGGAGGCCAAAGGGAGTGGAAACTTGAGGAGGTTACCGCCTGACCAACATGATGAAAACACTCATAT  
CTACTAAAATACAAAATGCATCAGGTGTGGTAGTGTGACTGTAATCCCAGCTACTTGGGACGCTGAGGCATGAGAATT  
GCTTGAACCCGGAGAGGGAGGTTGAGCTGAGGACCATGCCACTGCAATTCCAGCCTGGTAACAGAGTGAACACTCT  
GTCTTCAAAAAAAAAAGAAGTACCTGAGTAAGCAGGCCCTAAACAAGGGGAGGTTACAGGAGGCTTACAG  
AGGAATGCTGTTCCAGGCCAGGACTGGGTGAGGTTCTTATTTCTGTCACATTTCAGTTATGCTAGGATTTTATCTT  
CAGCTTGTAGTTCAAGGTGGGAAAGGGAGCCTCATTTTCAACAGACCCGGGCTGCTTATTTCATCTTCCCGC  
TGGGAGTCTCTCTGTGGTAGGGAAAGTGCAGTAAACCACTCTGTGCTCAGTTCTGTCCGCTTATCTGGCA  
CCAGAGTACCTACCTCACTGGGAGGGCTCACGAAGCCTGGCTGGGCGAGGACTCAGTAACACACTGCCATCGCTATTT  
TCATTCCAGTCTCTGTGGCTCATAAAATGGCTCCTTACGTTCTGCTAGAACTCAAGCTCCTGCTCCAGCTCCAGGACCA  
GAAGATGCCAGCATGTCAGTCCAGTACCGCAGCAGCACTTCTCACCGGCTCCTTCACAGAACTGG  
CTGCTGCCCTGGATGCCAGAGGGAGGGTAGTGTGTTCTGGCATTAAAATGGAAGATGAAGCAAAAAACAGATGTCT  
TTAATAAAATTGCACTGAGCTCACACTGGTAAAAACTCTACTGAGTTGACCAGTTCTGAGGAGTAGAACAT  
CTGCTGAGAATATGGTACCCATAAGCACAAGGAAAGGCCCTTCTGTAGAAAGGCACAGGGATGGTAA  
GAACATACAAATGACTTTCTGGTCAACTATTCAGTGGAAATTACAGTTCTGCTATAGCAGGTTCCAAGGATGCT  
TTGATTAGTGAACCTCCCTAGGAGCAAGCCATTAAACAAAGGGATAGCATGCAGAGGCAACCACAAGATGTCACCTG  
GTTCAAAGCTGATGAGGAAATAATGGCTGCTGAGAAGGAGCTGCCCAGATTAGGTTCTGCAGACAGTGC  
TTCTCAGGCCAAGAGACACCACACATCCAGGGCTCTGAATCCTTACCTTATCTATCTGATTACTCAGGGACATGT  
GGCAGTATCTAGCTAGAAGTCAACAGACAGAGGGTAGACCACCCCTCTTCCCTCTCCCTATGCTCCGTGAGCT  
CATGGAGTCAGAAACCCACGCTATCTGATTGGACTAAAAAGATAATGCCCTCTAAATATTATTCCATTGTTCAAC  
AATTATTGAATGCCCTCATGGGACAGACAGTGTAGGTTAGAGTACATCAGAGATATATCAGTGCACAAACAGACA  
AAATTGCTGCCCTCAAGAGCTACCATCCAGGACTCAGATTCAAAGATGATTAGGATTGCAAAGTAGTTGAGATCA  
ACACTCTGGTGTGTTAGATTAGGCATACAGAAATTGCGGAACCTGGCCACTATTCCATAACAGAGAAATCTAACGC  
CATGGCTTCCCACTGCCCTCCAGGCCACTTCCAGGCCACTTCCCTATACCAAAACCATCTCCGTGACAGGGAAACCTGTTCCATGAC  
TCCTATGCTAAAGAGGTTCAGAATAATGTTGCTTAATTAATGGTAGCATTGCTGTATGTTGATGGATTTTATCT  
AAATGGAATTCTCAAGTTCTCAAAGTGTCTACAAATTAGTGAAGGAAACAGGAGGTTCTGCTGATGAAACAAATACAG  
GAGCACATCGAGTCTGTCAGTCAACAGTCACATGTGCTCAAGCTATGTACCCAGGCTGACACCGCTGAGTGA  
TATGTCGCTCTCCGGAGGATAGTGTGGGAATCTCATGCTTTAGCTCTCAATTCTGCCCTTCCAGATAAACTG  
GCCTGAGTATATCCATTGAGAACTTCACATTCCATGGCTCAATTCTATCTCTCAACTCTAACTAAATTCTCC  
CAATTCTCAGTAGAATGTTCTACCCACAACTAACATAAATTCCACAGCAACAAAAGTGCACCGAACACTTATGCT  
ATAAGTAAGATACTGAGAAGAAAGTTGAACACAAAGAAAATTGCCCTCATGCACAAACATGTACATACATTCTTAG  
TTGCTCTTAATAGCAGTACTTTAAGTGTATTCTAGAAACATCTTAGTATTACAATAGCGTAGTTCTATTCTATT  
TTCATTCTAGCTGGAAACAGCCATGACATTCTGTTCTGGATTCCCTGTTAAATTGTTGCTGTTATATTACTGCAACAAAG  
GTAGAGTATATTCAAGAGATAATCATGTAATTATGTTAATCAGGTAGATACTTCAACACACACACACAC  
ACACACGCACACACGCGGTGACATGCACACACACAGTACCCCTCTCCCCAAAAGAGTAATTAACAGTGTAACTCCT  
TTGGCAACACAGTAATCCCTGATTGCTGGTTGTCAGTTACTCTCTGGAAAGTCATTAGATACTGTCACAACCTCAT  
CATGTAAGCTAAACCTCAGAAAATGTCTGCTCAACAAACTCTCTATTGATCAGCAGCTCCTTTTTTTCTT  
TGCTTCCAAGCAGTGTGAGACTGCAACACCTGTACATCATGGGCAAGGGCCAGAGGACGCATCTCAGTACCTG  
AACCCCTAGGAGCTACAGCTCCAGTTCCACTGGGTTCTGGATCTGACACCTGGGTATATCCACAAGTGTCTA  
TGCATCGTTAAATCCACAGTGTGTTCAAGCATTAGAATGTCATCTGTTGTTAAGGAGCAGCAAATTGCAATG  
CTAATTCAAACACAAACCATGCGGGACACAGACTAAGAACAAAGAAAACCTTGGAAATGCAATTACAATTATCTT  
ACTTTAGCCACAGTGCAGAGTGTGAGTCATTAAATTGTTAATATTCTATATACGTTGAATTCTGATGTAGC  
CTTATTGTTGAAAGAAAAATGTATATATGTTAATATTCTGTTAATCTGTTGTTCTTATTATCATAC  
TTAAGTTCTAGGGTACATGTTACACATGCAAGGTTGTTACATATGTTAATATGCGCCATGTTGGTGTGCTGCC  
TTAACCTCGTCAATTACATTAGGTTATCTCTTAATGCTGTCCTCCCACTCCCCCACCCTGACAGTCCCCGGTGTG  
TGATGTTCCCACTCTGAGTGAAGACATGCGGTGTTGGTTCTGCTCTGGCATAGTTGCTGAGAATGACGGTTTC  
AGCTTCATCCATGTCCTACAAAGGACATGAACATCATTCTTTATGGCTGCAAGTATTCCATGGTGTATATGTGCC  
CATTTCTTAATCCAGTCTACCAATTGATGACATTGGGTTGTTCAAGTCTTGCTATTGTAATAGTGCACCGCAATAA  
AAGGATTAATCATGCTGCTATAAAGACATATGCACACATATGTTATTGCGGCAAGGATGTTAATTTAAATGAA  
CATCTATGACTAGGTTCCAGAACTCCACTATATATTCTTACTTTTATTATGTTAATTTATATAAAGAACCTGA  
ATCCTAAGTGTAAAGTGCAGTAAATATTCTGTGAATATATTGAGTAACCACCACTGACAGATAAAATATAATATT

FIG. 7B (2 of 15)

CATTATCCTCTCAGTTACAGGGCCCCCTCAAGTAACCACTATTCTGACTCTTATTATTAGAAATTAATACTGCCTGTT  
GTTGAATTTCATAGCTTTGCTGAATGTTGACTGTGACATCCTTACTGTGGTCGATGTGTCAGTATTCACTTTT  
TTCAACTGTATGTCATATTCTTGTACTATAATTCTCTTGTAAATTGACATTGGGCTGCTTCTATTGTTGGG  
TATTGGGTATTATGAAAACAGCTCCGTGACATGCCCTGTCATGGTTTGGGTGGACGTTAGAACTCATTCCTTGGG  
CTATAAATACAGCTATTTCATTTAATATACTGCTCTGTAATAGTTAATAAAATATGTGTACATGGCTTAACAAA  
TGTCAAAGAATATACTGAGCTAGGAAAAGAGCAAACAAGTCAAAGCAGGAAGATGGCAGGGATAACAAAGGTG  
ATAGCCAAAATAATGAAAATAAGAAAACAATCAGGAAATCGCAAGATGAAAAGCTTGTATTGAAAAGAG  
CAACAAAATTCACCAATCTTAGCTGAGCTGACCAAGAAAAGGAAGAAGACTCAATTACTAAAATCATAATTGAAAGA  
TTCAACACAATCATATACAAGAGACCTACAGAAAATAAAAGGATTATAAAAGAATACGATGAAACAATTGAAAGCCATC  
AAATTGATAACCTAGATAATGGATAATTCTTAAAGGTACAAAGTACTAAAATTGACTCCAAGAAGATATAGAAA  
TCCAAATAGACCTACAGAAGTAAAAGATTGAGTTAGTAATCAAACCTCCACACACTACTATGTACCCACACAAAT  
TAAAAAATTAGGCTGGCGCAGTGGCTCATACCTGTAATCCCAGCACTTGGTGGCCAAGGCGAGTGGATCACCTGAGG  
TCAAGAGTTCAAGACAGCAGCTGGCAAGGTGATGAAAACCCGTCCTACTAAAATACAAAATTTAGCTGGTGTGG  
CGGGACCTGTAATCCCATCTACTCGGGAGGCTGAGGCGAGAAGAATCATTGAGACTGGAAGGCAGAGGTTGAGTC  
CAAGATCATGCCATGACTCAGCTGGCAACAGAGCAAACCTCCATCACAATAATAATAATAATAT  
TTAAAATTTAAAACCTCTCAATAAAAGCTCAAACCTGGGCTTACTGATGAAATTCTACAAATATTGTTAAAGA  
ATTAATCTAATTCTTACCAATTCTCCAGTCTTCTTCAACGAAATGAGAAACTACAGGCCAGTATCTGATGAAATAGATGT  
GAAGCTAGCATTACCTACTAAACAGACAAAGACATCATGAGAAAACACTACAGGCCAGTATCTGATGAAATAGATGT  
AAGACCTCAACAAACACTAGGAAACACTGAATCCAACAGCATATAAAAGGATTATAACCATGGCTAAGTAGGATTATC  
TCAGGAATGCAAGATAGGCTGATACCTGAAAATCAATTGTTGACCATTTAATAATAAAAGGACAAACCCATACAA  
TCATCTTAGATGCAAAGAAAAGCATTAAATAACGCTTCTGATAAAAACACTCAACAAACCTTTAG  
GAAATAAGAGAACTTCTCAACTTGACTIONGGCCTTATGAAAATCCACAGCTAATGTGACACTTATTAGTGA  
CAGTGTATTATCCTAAGATTAGAACAGACAAAATGTCTACCCCTGCCACTTCTATTCAACATATTAGGAGTTCTAT  
CTAGGGCAATTAGGCAAAAAATAAAACAAAGACATCTAGGCCAGGCGTGGCTCACGCCGTGTAATCCCAGCATT  
GGGAGGCCAAGTGGACAGATCGCTTGAGGCCAGGAGACTGAGAACACCCCTGAGCAACATGGCAAACGCCATCTC  
AAGAAATACAAAATTAGCTGGCATTGGTGGCTTGTGTTGAGTCCCAGCTACTTGGGAGGTTGAGGCTGGAGAATTG  
CTTGATCCCAGAACAGCGGAGGTTGAGCTGAGATCACGCTACTGCACGCCAGCTGGGCCACAGAGTAAGACCTG  
TCTCAAAAAAAAGAAAAGAAAAGAACATTTAAATTGAAAAGGAAAGTAAACTATCTCTAT  
TCATAGGTGGCATAATCTGTTTATAGAAAACCATAAGGAATCCACAAAACCTCCATTACAACTAATAATGAAATT  
CAGTGTGCAATGGTATAAGATCAACATACAAGAATCAATTGTTCTATACACTACGATGAGCAATCTGAAAATGAAA  
TTAAGAAAACAATTTCATATAAAATAGCATCACAAAGAAAATTTAGGAATAATGTAACAAAAGAACACAAGAGT  
TATACACTAAAATGACAAAACACTGTTGAAAGAAGATAATAAAATGGAGGATATCATATGTTCATGAATCAGAAGA  
CTTATTATTTAAATAGCAATACCCCAATTGATCCATAGATTAATGCACTTCTCTCAAGAATTCTAGTTGCTTT  
TTTTTTGGCAGAAATTAGCAGGACTCACAATTCCCAATTCTGAGGACTTCAAGGGACCCAGTATAGCCAAAACACCT  
TGAAAACAAGAACAAAATTGGAGGACTCACAATTCCCAATTCTCAAGGACTTCAAGGAAAGTAGTCAAGACTATG  
GGGTTGACATATGAGACATATAGATCAATGAAATTGGTTAGAGTCCAAAATAATCTTCTATATTAGTCAA  
TTGATTTTGACAAGAGTGCACAAACATCAATGGGGAAATAGAATTTCATAAAATGGTGTGGGACAATGGGTA  
TCCACACTCAAAGAATGAAGTTGGACCCATATTACACTGTATACAAAACACTCAAATAGATCAAAGACCTAAATG  
TAAGAGCTAAAATGTTACATAAAATTAGAGGTAATCATAGACTTAGAAAAGGAGTGGTTCTAG  
ATATGACACACTCGAAAGTATGAGTAACAAGAAAATAGATAACTGGACTTCAGTAAAATTAACTTTGTGATTT  
TAGGACACCATAAAAATGAAAAGGCAACACACAAAATGGGAGAAAATTGCAATCAAAACCTAATAGGGACT  
TGTATCTGAAATATATTGTTAACTTACAACCTCAGTAATAAAAAGACAAATAACTCAGTTTTTAAAGGCAAAGA  
TCAGAATAGACATTCTCAAAGAAGATACGCCATAAGACCATGAAGATGTTAGCATCATTAGCCGTAGGGAGATGC  
ATATTAAATCACAATTAAACCACTTGTATACCCACGAAGATGGATATAATAAAAAGACAGGTAATAAGTGTGGCA  
AGAATAAAATGGAGTCTCAGACACTGCTGGGAATGTAATGGGAGGCTGAGTAAACACTTGTGATTT  
TCTAAAGTTAACAGAGGCTGGCGCTCGCGGCTCACGCCCTATAATCTCAGCACTTGGGAGGCTGAGGCTGGCAGAT  
CATTGAGGCCAGGAGTTGAGACCAAGCAGCTGGCCAAGATGGTGAACCCCTGCTCTACTAAAATACAAAATTAGCC  
GTGTGGTGGCAGGTGCTGTAGTCCCCTGACTTGGGAGGCTGAGTCAGAAGAATTGCTGAAACCCAGGAGGTTGG  
GCAGTGAGCCGAGATCGTGTATTGCACTCCAGGCTGAAACAACCTCCATGTCAAAAAAAAGTTAAACAGACAGTT  
ACCATACAAGGCCAGCAAATGACTCTGAGGTATGACCAAGAAAAGTAAACACTTGTATACACATCTCAG  
CAGCGTTGGTAAGTCACAATTAGCTAAAAGCAGAAACAATCAAAATGTTATCAGTTGATGAAATGGATAAAATT  
TGGAAATTATTAGCAATAAAAAGGAATGAGGACTGCTACAATATGATAAAACATCATGCTAAACAGC  
AGACCCAGGGTTAGAACACAGGCAGTCTGTTCTGAGTTCTATAGTTCTATCCTGATTGCTGTTTCCAGGGTTAG  
GAACACAGGCAGTCTGTTCTGAGTTCTATAGTTCTATCCTGATTGCTGTTTCCAGGGTTAGAACACAGGCAGT  
CTGTTCTGAGTTCTATGTTAGTTCTATCCTGATTGCTGTTTCCAGGGTTAGAACACAGGCAGTCTGTTCTGAGTT  
CTATGAGTTCTATCCTATATTGCTGGTTTCCACAGTCACCTCATTGCTTAGGAGCAGTTCTCATCCTGACTGTT  
AAGAGCTTTAGTCATTCCTTCACCATACACCTCTGATTCTGTTGCTAACAGAATCAGCAAAGTACAAAGG

FIG. 7B (3 of 15)

FIG. 7B (4 of 15)

FIG. 7B (5 of 15)

FIG. 7B (6 of 15)

FIG. 7B (7 of 15)

CTATTTCCGGAGTCTGTTTGCCTCTGGCAATGTTGCATCCTCATTCTCAGAATCTTCTCCTCTACATCAA  
ATCGTCCCTCTCATTTCATCTGACCATACTCCTTAGTCCATCATTATAGAGGTATTCAACCAACAAGACCAAT  
CAAACATATGGCAGTTAATAAAAGCTTCACTGCCTCACCCAATGAAATGACTCTAGTGGTAGAAATTAGGAGGCC  
TGGCAAGCTGGCAGAGGGAAACGGGGATAAGACAACATTCTGTGGCTGAGTTACCTGCCAGGGCTCTAGATCAAGCCAT  
AGTCTCTCCCTGTTTGTACTGCAGGCTCCCTGGACCTCACTGTTGGTTTATAATTAAAGATAATGATTACAAGA  
GGTCTAAATCTGAAGCCCTGGGAAGATCCAGGAGGCTCTGAGACATGAACTCAAGCTGAGGTCTAAGCTGCTT  
CCTACTGGTATAAAATCCCTGATATTCCAGAGTAGAGTTAGAACTTTCAAGGTTACAATAACTGAAACTGGTCAA  
ACTAATTAAACAAAATGTTGGAGATAGAGATAGTATGAGGATTAGGAGATTCTGGATCTCAAGGGCCAACACACA  
TCCAGGTCTCATAAACTCCTGGCTGGGAAGATGAAAACACTACAGAGTCAGGTCTAGATGACTCCGCCATCCCTAGTCTC  
TGCTGCCCTCTGATCCAACCCCTCCATGGCTTCCCTGCATTCAATGTAATCTTAACCTTCACCTGGGACTACAAA  
GCTAAGATTATTTGAGGCTACACTTTGCAAGGTGGAGGAACCTCTGTAACTGTAATCTGAATAGCATCTTATATGACACAG  
TGAAAATGAGGGAATTTCAGGAAGATCCTGAGATGCTTATGGATCTCATGTAACAGGTAAGCTTCTGACACACTCAAGG  
GACACCATTTGGGGCTCGAGGATTGTCACTGTTAGCTTACTAATGTAATGATCACAGGTAACATGGATATAGTGT  
TTGGATGATAGCCAATAATATAGAATAATTAAACATTAAATATAACACTATCTTCACTTACCC  
CTAATTAAAGTGAAGGATAATAATTAACCTGTTATAGGAATTATTTCCATATGCTTGTTCAGGAGAAATTACTA  
TATAGTTTACTTTAGAAATCATTTTACGCTGAGTTAAAGCTGGTCTCCAGTCTGTTGAGGAGAAATTACTA  
CAGAGGCAAATTGCGCTGAGAGCATTAAAGACATCATACAAAGGGCAGTACTTTGCTCTGTTTATTGAGGAGAAAGGAAAG  
AAAAGCAGAAAATTGCGCTGAGAGCATTAAAGACATCATGTTATCAGGTTTTCCCAAGGCTTTACTAA  
GTACTATTTCTGGAGGTCAAGCACAGCTAAACATGAAATAAAATAGTTGGACTAATAATGTTTCTGCTCGTT  
TTCTGAAATATAGGCAAATCTCAGGGAGGGTACAGGGAACTCTGGGGAGAAAAAAAGAAAAGGTACACAAAG  
TAGAAGAACAGTCTCATTAACCACTGCTCTAAACTACTTCTCACTCAATCTGTCTCAGAATTGCCAAGAGTTACCA  
GGCATCTCCTGATCGCGCTGACCTGGCTCCAGAACATGGCAGAGAACACACCAAGAAGAAGTGTACACGGAGGCTG  
CCATGTGCGTGGTCACGCCGTCGCTTAGTGGCTGAGTATCTGAGCAGTGGCTACCTGCCGTGGC  
AGTGTCACTCCAGGTAGGGTGTGCACTGCTTCCCTAGAGCAGTGGCTCAACTGGGCGATTGTCAGGAG  
CCCAGGGACATTGGCAATGCTAGATAACATTGGTTATCACAACGGGATGGGTGAGTAGGTGCTACTGGCATCTGA  
CTGGTAGAAGCCAGGATGCTGAAACATTCTGCAATAGGAGAGCTCCCTGACAAGAATTGCTGGCCCCAAATGTCT  
GTAGTGTAAAGGTTGAAAATCCAAGTTCATACATTACATTGCTTCTCTAATTGCTTCCCAGTCGCTGGGTTT  
TTTAAATTACTGTTACAATAATGGCACCTAGCATTATAATGCACTTTAGGAGACATTGCAAACACTTCACTATG  
CATGGCTTCATTTGAACTCCCCGTAAGGCTGTGAGGAGGTAGGTAGGGAGGGTATTATCCCACCTCGCGGATG  
AGAGAACTGAGAGAGCAAGTTCTAAGGTCACTTAAACTCTTCAAAGACTGTAGTGCACACAGTACTGACATT  
GTGAAAGTTGGAAAACATTGATAATGATTTCCTCTGGGCCCATTCTGATTGACTTCAACCTTATAGGGC  
CCACTCTCAATCAGGAAACATTGGCAAGGGAAATTGCTGCAAGACCTAAAGCTGGCTGGATGGGATGCTCAG  
GATAAGCTGAAACATTACCCACATTGGCAAGGGAAATTGCTGCAAGACCTAAAGCTGGCTGGATGGGATGCTCAG  
TGGCCACTAAAGTGTCTACTGAATGTTAATGTTAGAGAGAGAGAAAATAAAAGCACAATGTTGGGACT  
TTTTGTAAGAGACATAGTTGAGAGATGACCATCCCTGAAACCATGAACAAATAGCTACAGTAATAGAGTGT  
CAAGCCAGACTACGAAGTCAATTACAAGGGTTGATTATTCTGTTGAATTACATGGCTGATTGAAAGCTT  
TGTCTGTTATTGTTCTCAACACAATTGTAATTGATGTTGATGAAACAGAAAGAACATTCAAAGTAGCTT  
AGGCTTAGAGAATAAGTCACTGAAACTATGCTGGTGCAAGCCAAGAGCTCTGGTTCCAGAACACAGCAAAGCTGG  
TTGCTCTATGAATAACTCCCTTCTATGGCTCTCAAGAACAAAATAGTCAATTCTGTGATTCTCATGCTGGCAA  
TGAATTCTCTTAATTGAAATGTTTATAAGCTGATAATTAAACATCCAAAGCATAAAAATAACACCT  
GATTCAAATCACATAGAAGTGTACAAGAAAGTTATTAGTACTACTCTTCAATTCCAGGAAATTGTAAGGTTAGCACT  
TGACCATGTGATACTATCAGGAAATTATGTTACTCTTCAATTCTGTGATTCTCATGCTGGCAA  
TATTGTTCTTACTAAATTATTTACTTCAATTCTGTGATTCTCTTCAATTCTGTGATTCTCATGCTGGCAA  
AAATATCAATTGCAATTGACTTATTGACTTATTTAGTAAGCCTTAAGTCAATTCTGTGATTCTCATGCTGG  
TGCTAATAATGACATGCCAAGTGAATCATTACACAACTCAACAGAAATATTCCACATTATCCGACATGGGGCATA  
CAGCTCTATCTGTCACATATTATCCATTGATCTCTTCTGAGGAAATTATTGTAATTCTGTGATTCTCAT  
GAACGTTACATTCTAACAGAGAGACGTAATAACTAATTCTCAATTGTTGTCAGTTAATTATGAGAAATACTG  
TTATAAGAGGCAAGATAATTGAGGCTTGTGAGGAGGCAATTGAGTTAGGTGTTGTCAGCTACAGAAGAGAAG  
AGGCAGAAGAACTGAAGTGTAGGTGAAATTCTACTCTCTCAATTGGACATACAAATCAATTGAAATGTTAGCTGG  
CCAAATTATTAATGTTGAGGAGGAAACCCAGACTGACAGAAGGAAATTGAAATTTCAAGCCGTCAGGAAATGTTAGCTGG  
CAAGTGAAGGACACCAACCCAGACTGACAGAAGGAAATTGAAATTTCAAGCCGTCAGGAAATGTTAGCTGG  
CTAGCACCTGCCACTGGACCTAGGGCCAAACAAATGTCAGCAGAGCTCACTGTCATCACCACCTCCATCTGCCA  
TCTGTTGTCAGCTCATTCTCACAGGCTTCCCACACCACAGTTAGGTTACATCTCTAGGTTCAAGTCTAGGAGAG  
AAGAGAGATGCCCTTCTAGCAGTTGAGGAAAGCTCAGTGACATCTACTGATCCTGCTGAAACATCTGATCCTGT  
GCTCATCCCTGAACCAGCATACTGCCAGAGAAATGAGTGTCTGATTACTGACCCGGTCATGGTCCACACCTG  
GAATTATGGGTATTCTCCCTAAATCAGGATGCCATTACTTATAGAAGGAGGAAAGAATTCTAGACAGCATTAACAA

FIG. 7B (8 of 15)

CAGATGTCAGTGTGATTTGCAAATGCTCTGCTTTAATTTCAACCTGTTCTGCTCAATGAAATAGAGCTTGGAAAAGATTTATAAAACTAGAGATAAAATATGTGCAAGGAAAATAACTTGGAGGTCACTGAATTCCAGGAAACTGAGA TCACTGAAATTCTGTGTCAGACTGCAATATTATTTCAACTGTAGATACGGACACATTCTAGATACTGCTGTAC TTGTACCTCCCTGATCCTGAAGCAGAAAGTCTGAGAATCCTTCTGACTACAGCTAATGAGGCTACATAGCTT CAAATCTGTCCTGATGAGAAATTGCATACATTCTAATAGTATTAGTATCTGGGTTATTAATGCTTCAACTGAA ATTTCTTGGATCTCTGTCACAGAAACATCATAATACATAGGGCAGGTTGGAGAGAAAGACTGGCCACAAAGGGCTT GAGAGCCTCTATATTCTAAACACTACGTTACAGTATGCTAGTGAAGAGATAGGGCTATCTATGACAACATATGCTC TGACTGATTGCTAAGGGTATTGATCAGATCTGTCACAGGAGGAGACAGCTTGTACAGGCTACAGGCTTGTACAGGCAACTC TGATCAGGTTAGTGTGGCTACTGGAGAAACTATGCTTAAGAATTTCGAGACTATGCTTCAGGCTCTGGGAAAAGTGTCA CAGTTGATTAGTTATGCTGCGCATGATTACAGCAATAGGAAGGAGTGGCATGTTGCCACCTGTTGTAATCCCTAAACT GGGAAAGGTTCCCAATTCTCTGTTTCTATGATCTTCATAGCTGTGAGCTAGGAAGAAAATGATTCTGACCT GTCACATATTCACTGCCAGGGCAGTCTAGGGTGAAGAGGCACTCACCTCAGGGTCAAGCAGGTTACAAGATCAGTACT TCCATGGCCCTAAAGCAGTACCTCTCTAAATTGTCTGGGTTCTCATTGGTCAACCCAAACATGGCTCTGCA TGCTCTGCTAGAGGCTTAACGCAATAGTTATGTAAGGAAACAAATGCTGGAAACAAAATGTCAGGAAGAACAAA AACACACACACAGTAACGTGTCATGCCATGAAAACCTCTTAATGAAGACAGCCTCGCTTGCTGTTGCTGATGTCAT GGCTGTTATCTGACTCACTCCAGAGTAGCAACATACTTCAGAAAAACACCAGTGAAGTCAGAGGTCACCTCGGTGAA ACAGGGAGCCTAGTTAATGTAATTGGGTTCTGCTTTGAAAACCAGGACACCAGCCCTATGTCCTTAGGGTTCTT CACTAAAGTAACCTCAGCTGTTGACATTGAGGTAAGTGTCTTATACAAAATCTCTAATGGTAAAAAGAAAAGCT GAGGTTGAAGACCAGTGTGTCAGTGCCTCTCTAAATGAATGGCAGACAGATACTCTGGGGTAGAATTACAGACCT AGTTTAGTCACGGTCTTGGTAAGGATCTGACACCAGCTTCCTCGTTCCCTGTTGGTCTTACTAG TCTGGTCGCCCTGTTCTCAGGCTTAACTGTGTTCTCTCAGAATATTCTTCAATGTGCTGGAGGAGTGTGTTCTC TCTGAGGACACCCCTGTCACCTGACGGGATGGGGTGTGCCAGGGCAGTACTTCACCGAGACTGCCCTGGTACGGCTCT GGAGCAGGCCGCGGAGCTTCAACCGTCAGTGCCTGGGGCATCCGGGCTGGCCCTACCTCCAGCTGGAC TTGGGGTCTGGGAACACCTGGCTTAATGGCCAGTCAGCCCCACTTCCGGAGGACACGTCAGGGTGTGCGGGCAG GGGATGGCCCGGGGAGGACTTTGATGATGCAAAATTGCTAGGATCTCCAAGGGAGCTGAGATAACCTTCTACAGT GCGCATCTGAGCTTCACTGTATGTCATTGGTCTGGGAGCAGTTTACAGTATTATTCTATTAAATAGGGTGGAACTA AGCCACAGAGAGGTGAAATGGCTGCCAGGGTACACAATAATGATGAGGATGTTTCACTCCCTGTTTCTCT CAGAGAGAAAAAAATTAGGGAGGAACCACTGGGAGGAGAGAGGAGGAATACACAGACAGTGTCTCCCTCTAGCCACTG TGCAGTCTGAAAGGACCATCACAGACAGGACAGCTACAGAAATGTGGGACAGAAAACCACTGAGACTCTCTGGTTAA CGTAATCTGGATCTAAACACTCTACTATATATAGAAAATATAGAGAGATGAGTCATTGAGATTCAAGGCAAAG GAGGAAACACTTTGCTATTTCTTTGAGACAGAGTCTAGCTCTGCCCCAGGGTGAATGCACTGGTG CAATCATGGCTACTGCACTGCCATACCTCCAGGGTCAAGCAACTCTCTGCCCTAGCCTCATGAGTAGCTGGATTACA GGTGTGCAACCACACTCGGCCAATTGGTATTAGGGAGACAGGATTTCAACCTGTTGGCCAGGTGGTCTCA AACTCTGGCTCAAGTGTCTGCCATCTGCCCTCCAAAGTGTGAACTACAGGTGTGAGGCCACACGCCAACTT GTTTCTATTAAATGTCCTCTCTTACATTAAAGCCAAGAAAGTATTCTAGTTACTATATTAGCTGACC CAATTGTTTCTACTATACACTCATCTTCTTCAAGGTTTCTCTTCAAGGTTTCTCTCTACAAATTATTAA TTTTAAATTGTTTACTGTCCTCTCTATTCTGTTCTCTTCAAGGTTTCTCTTCAAGGTTTCTCTCTACAAATTACTCTCAT TTTCTCTCAAACCAAAATGAAATTAGAATCTACTAACTTCTGGAGGCACTACATTGAGTCTGGCTAGGGAGGA CCTCTGTAAGGAAATTAAATACACTAAACTGCTTCTGTAATTGCTGTAGTCTCTGCTACCAAACCTCTCTGTTT TTCTTTCTGTTTGTGTTTGTGTTTGTGAGGAGCAGCTCTGCTTGTACCCAGGTGGAGTGCAGTGTGATG CAGCCTGGCTACTACAGCCTGACCTCTGGCTCAGCTCCACCTCAACCGCCAAGTGTGAGGCTACAGGAGC ATGCTACACACCTGGCTGATTTTAAATTGAGGAGATGGGGTCTCCCTAGGTGTCTAGGATGATCTGAACTTC TGGGTTCAAGTGTCTCTCTGCCCTAGCCTCCAAAGTGTGTTGGATTACAGGAGTGTGAGGACTCTGACTCAGCCAGTATT TTTTCTCCCGAAAGCTCTCTCTACTTATGCCATACAGGACTACTTAGCAGGGTGTCTAGTTCAAGTGTGAGGCTT ACCACTGCCCCAAAGTGTCTGAGATACCCCTTCTGCCCTGTGAAATACTGTGATACAACAATAATTCACTCTCCAGCA CATTGTTGGACAATGACCTCTGGTTGCTCTTCAAGTTCAGTGGATTAAATTCTCTGATGCTCTCTCTTT CCAAGGGAGGCTTATAGAGACAGTTAATGAGGCTACAGCTGGTACCCCCATCTAGAAGCGCATCGAGAAATTCCGAA AGCTGACACTCACTCACAGCAAGCTGCAGAGAGCCTGAGCAGCATCGTTAACAGGTAGCCGGGAGCCTGGCTGGCA GGTCTTGTACCTGGCGAGGCCACCTGCTCTACAGATGCTTAGGCCATCTCTCTCCAGGGAGTGTATTATCTTTA GCACATTGCTTCTGCTCACCTGCTAAACAGAAAAGGGCTGAAATTCTCTAAGCAGGAGCAGGAAATTCCATATGTGAA AACATACAGCTTAAATTACTTTAAACAGGAAATGTGAGGAAATTCTTAAAGTGTAAATTAAAAGAAGTCCCGAGAAATTCTT CATGGGATTCTTTGTTGTTGATGAGTATTCTGAGTTTCTGAGGTTTCTGAGGAGTAAATTCTGTTTACAT CAGGGCATAGGAGTAAAATGCTTGTAAACACATGAGGAGACCCCTGCCCTTGCAACTCAGTGGCTCTCAGGATGACAT AACTAAGGAGAGCTTTTATATTGTTGCTCAGGATCATAGAGAATGTTGAACTACTTCCGAGTTGGTTCTT GATCCAATTGGGAGTGTGATGAAACAGGAGTTGTCTACAAAGAGCCTGCAATTACCAAGCTCTGAGATCTCACAT AGACTAGAGGTAAGAAAAGTGTATTCTGTCGCGCTGACCTGGTACACTTACAAAAACAGTTAGAGTGGGTACATCACAA AAATAACAAATGAGTTATGAGTTATGCACTCATCATTGATCTACATAAAGTTTCCCTTGCAATTAAAGGCAAAGT

FIG. 7B (9 of 15)

FIG. 7B (10 of 15)

FIG. 7B (11 of 15)

AGCCTGAGTGCAGAGTAAGACTCTGCTCAAAAACAATAAAAAGAAAATAATTGGGCTGTGTATGGTGCAC  
GCCTGTAATCCCAGCAATTGGGAGGCTGAGGTGGTGGATCCCTGAGGCCAGGAGTCAAGACCAGCCTGGCAATGT  
GGCAAAATCCCATCACTACAAAAAAATACAAAAAATAGCCAGGTATAGTGGCACACACCTGTAGTCTCAGCTACTGGGAG  
GCTGACATGGGAGGATCACTTGAGCCTGGAAAGTGGAGGCTGAGCAGAGATCATGCCACTGCTCTAGCCTGGG  
TGATAGAGCGAGACCTGTCTAAAACAAAACACACACAGGGAAAATACATTACTTCTGAGTGTTC  
CTCTAAAACCTCAGATTCTCTCTAAGAAATCAAATTCTGAGATGCTCAAGACCTCCTTATTTTTTGTTTATT  
CAAACCAACTACAAAATTAATGTCAAACTAAGAAGTCACTCCAATATTTCTCCAAGCAATTAAATTCTCTCATAT  
ATGTATGAATATTATCATATATATGTGTGTATATATATACATATATGCAATACATACATATGCAATACAT  
ATATATGTATGTGTATATATATGTGTGTGTATATATATATATATATTCTTTTTTTTTTTTT  
TTTCCCACAGGGACCACTGGAAGTAGGCCAAAGTGTGTTGGCTGAAATTCTCTGCTGATCCTAAACTCTGACATCAC  
AAACAAGTGTGAGGTTATGCTTAAGGAATTCACTCATGAGGTAAAGAAGGGAAATGGCTGGAAATTCTAGTAGAGCAGTGGT  
CTCAAAGTGCATCTAGACCAGCAGCTCACCTGAGAATCTGCTAGAAAGACAAAGTCTCAGGCACCCCTCAG  
ACCTGCTGAATTGGAAATCTGGAGGTGCGCTCAGCAATGTGAGTTAACCGCCCTCCAGGTGATCTGATGCACAC  
TGAAGTTGAGGACCACTGCAAGCAGAACACTACTTGAACTACTAATGAGTAACAAACGTCAACTATGAAACGCTT  
TTGTCAGCATCCGTTGCTCACAATCACTGTTGAAACAAAGTATCATCATCTCCCTCATTTACAAAAGAGGA  
ATCAGAGGTTCAGAGAGAGGGAGATAATTCTAAGGTACACAGACAGTGGCAGCAGAGATGAGCTCAAACCCAGGTC  
TTCTGAATCCAAATAGTCCACATGTCATCAATGTGCTGATATTCCACTGATGCACTAGAGTCCCAGAGGTTCTTGCAAT  
TGGCAGTCATTGTAATGTTACAAATCTTATAATCTTATTAGAAACTTAAACATACACTGCCTCAAATTGAGAG  
AGGCAAGTTCTAAACCAGGCTTTCAAGGTATTCTGTCAGTCTCCCATGTCAGACAAGTCTCATCTGTTC  
TTAATTCTGCACTGGAGCTGCTTCAGACAGTCAGTTAGGAACACTGGCTTTGGTCAAAGCCTGTAATTATTGCAA  
TACAGACAGATATATTGGGCTCTATGGCTTAAATAGAGTATGAGGATGAGTGGCATTACCTATAAGAGAA  
AAGGACTTCAGAAAATGTGAGCAATATTCTTCTATTCAAAACCTAGAGAAGAATTTAGTATAAGAATATCTC  
ACTTGGCAGATGGGATAAAAGGAGACTAAAGCTTGTCTAAATTCACTGAAACTCTCATCAAAATGCTAGCATTGTGAGGT  
TAGAGATATCTCCTCTTCACAGGCTTTGCGAGAGGCTGCCAATTGCTGCTGATCATACAGGAGACACACTGTGCCCTGC  
AGTGAATCACGCCGCTTGGTAATAGGATGTTGTGTTGGCTTGGCTTGGTATTGTGCTGATGTCAGACATACTCA  
CAGATTCTTGAATTGTTGATTGTTGATTGTTCTGTTGCTGATTTGACAACAACTCTGACAGAAAATAGTGTG  
TTGTTGTTTCTAGTACATAACGTAATCTTAAAGGCTAGAAAATATTGGGAAATTATTATTATTATTATT  
ATTGAGACAAGGCTCACTGTTGCCAGGCTGGAGTACAGTGGCATAATCTCAGCTACTGCAACCTCCACTTCCC  
AGGCTCAAGAGATTCTCCCTCCAGCCTCCAAAGTAGCTGGGACTACAGACGTGTCGCCACCATCTGGCTAATT  
TATTTGGTAGAAATGGGTTTACCATGTTGCCAGGCTGATCTGAACTCTGACCTCAAATGATCCACCTGCCTG  
GTCTCCCAAAGTGTGGATTACAGGCATATACCACCGTGGCCGGCCATTTTTATTGGGAGACAGGGCTCA  
CTATGCCGTCTAGGCTGGCTTGAAATTCTGGCTCAGAGATTGGGGCTTAAAAAAATTCTCATATTATT  
TAAATTCTATTATGGTGAATGCTTCAAAAGTTGACTATGCCCAAGGACCTCTAAAGGACCTATGAAATTGTTGAAGAG  
CACTCACTATATTCCAGGCTGATATTAGTTAGGACTACAGAGATCTGGCTTCTGTTCTTAATGACAGGACA  
TAGCCCTGCATGGCTGAATAATGAGATGCAAGCAGCATATGCACAGAACTTAAAGAATGACTAACTACAGGACTATAAGATCA  
GAAAAGAGAAATCAGTTCAAGGCTGGAGCATTGTGGGAGGCGTTATGAAAAACACCAACTTAAATCTGCTTACTAT  
ATACGTTGGAAAGAGGCGCTAGTGGGAAGAGGGAGGCCAGGACAGTGGCCCTGCTGATCCAAGGTATCCTCAGCTG  
CTTCTGTTACCCATGTTGAAAGTATTACTACATATGATATTCAAGAGAGAGAGAGACACATTACATAACTT  
TTATTCTCAGTATATTGCTGTAATTGTTGTTAACTCTTACTCTATTGTAATTGTTAAAGCTTATCATAGGTTGTA  
TGTATAGGAAAAAAACATAATATGTAAGGTTCTGGTACCTCCAGGCTGTTCTCATGAGCATGCTAGGACAAGGAGGAA  
TCCCGAGAATGAGGAGGACTGAGTACCACTGAGTGGACAGCAGGACACGAGACTCTGTCAGGAATGCTGTGATGCA  
CCGGGTTCTCTAAGTCCAGCTGGACAGCGTGTCTCATGAGCATGCTAGGACAAGGAGGAAAGATTGAAATATGATA  
ATATCAGTAATGAGGCTCTGAATACAATTAAATGTTAAGAAAATGTCAGGAGAGTGTGATTTCATTACTCAGTT  
TGCCTCAATTCTACTAGTTAAATCTGCAATCCAGTATCTCACGGGTATGATCTTCCATGACACCACCTAGG  
TAAATGTAATTACAAAATCCCTACTAAACATGCGTTCTCATTAGCTCCAGGCCAGGAAAAGTTACTCCAAAAGAA  
CCAGTGCCAGTAAACTAGTCCCAGGCAAGAGATACAAGAGGAAATGACTTCTAGGGGTGCTCCTTAACAAAGT  
CATTAGAGTTCAATAATGAGGCTATCATCTCCCTAGATGCCCTACAGAAATGTTGATTTCAAAATCAAATTCA  
TTTAAAGTTGTTCTCTACCTTTAATGGTATTCCACATGGAACAGTCCCACCTTCTCCCCACTGGCTGGGCTG  
CTGCATTGTTCTAGGAGGCCAGGAGACTGTCCTAGCTTCCAGACTTCACTGTTCTACACGTACCTGAGGATTGTC  
AAATGCAAGATTGGGCTGTCAGTGGCTCCGCTCTAAATCCGACACTTGGGAGGCTGAGGTGAAAGGACTGCTG  
GCCAGGAGTTCAAGGACAGCCTGGCAACATGGCAGAAACTCTGCTCTTTAAAAAAATACAAAAAAATACAAAAAATT  
GCCAAGGGCTGGTAGGGTGTGCTGAGTCCAGACTCGAGAGGCTGAGGTGCGAGGATAGCTTGAGCCCGAGGAG  
GTCAAGGCTGCAATGAGCCATGTCGTCAGCTGAGGACTCTGACACTCCAGCTGGGAGGAGATGCTGAGCCCGAGGAG  
AAAGAAAAATGCAAGATTGTCAGTTGAGGTTCTGAGGAGGCTGAAAGATTGCTTAATTCTCCCTTACATTCTC  
CTGCTGCTGCTACACTGGACAAACTTGTAGGAGGAGGCTGAAAGATTGCTTAATTCTCCCTTACATTCTC  
TATTACCTCTCCCTCTCCCTGAGGGCTTAATCTCTAGGCCATCCTTACATCATTACACTTTGCGCTGCTC  
CTCCAAAATAAATAAATAAATAAAATAAATAAATTTAATGGCAAAAAAGAAGTTGTAATCTCAATAAAAT

FIG. 7B (12 of 15)

TATGTGAGAACAAAAAAAGCAAACATGCTCAAACGTGCACCTGAACCAACTATAGACGTCAGTCATCCATTCA  
TTCAGCAGTTATGAGCTCTACTTTGTCAGGCACGTGCTACATATGTGAAGGGATGAAGTCCAATATCAGTAGGA  
CAAGGCTACAGACAAAACAGTACTGCTGCTCATTATTCTATCTCTATGTGCAAACACAAACAGATGGCCTGCCCTCCACTTC  
ATTCTACAGAGATCAGAAGTCGTTGGGTGAGACTGTGCTGATGGTGCACAACACTGTGTAATTACTAAACACTCATCAAACCTC  
TAAACATAAAATGGGTGAATGTTACGGTATGTAATCATACCCCTGAATACAGATAGTAGATGAGGTTCCCTGTTGCTTA  
ATTGCTCTCAAGTCAAATCTGGAAGTTACAGCTTTAATGAAATAGAGTAACATTCTTACGTTGTTGCTGTTGCTTA  
TTTCTCCTCCACTCTGCTAACAGACAGCAGAGGTGACGCAGAAGTGGAAAATATTGGGCTTAGATGATAAGCCAGATTCCAAGGTGACCATAAATG  
AGTCTCTGTTGCTGAGAGCTAATAGCGAACATTTGCTTGCAGGTCCACTGCGTCTAGTGCCACCACGGGCAGCGAC  
CTTCTGACTCAGCTGAGTAGTGAAGCAGAACAGCCATAAAGAATCTGGCAGCCTGATTGCTGCAGCCAGTACTCATC  
CAGCCAGTCCTGCAACTCTTCAAACGTGTTACCAAGCTGGGACCTCAATCAGCTCTGCTTTCTGCAATAATAAAAAA  
CATCTCGGGTTCAGAAGCCAAGACAAGAAGATAGAGAGATAACATCTCTATCTTCTCTGCTCCCCAAACACCC  
GACCATTAGATTAAATTCTTAACTTCTTAACTTATCTGGACTTCTCATTCTTAAAGACTAAGTGTGTTAAATT  
TGTTTTAATTAAATAAAAGATAGTAGTACTCACTGGCACCAAGTACAGCTTGCCTTAAGAGAAGTAGTTTCAAGATA  
ACCCCTGAAAGGGTTCTGCAAGCATATAATGTGGTCAAGGCTCAGAAACAGGCTGGTGTGGCGTTTAAACTGG  
GTTGGGTCTATGAGAGGAGAGGAAATTGTCAGACTGCAAAGGACAAAGGACACCAAATGTGAGGTGAGGTGGAA  
AAAGAAGCAGTAGTTAACTTGAGACCAAGGCCATATGCGCTGGCTTATGCTGGAAATGGGAAATGGCTTCTAGGC  
AGTATATGTCGGCTTGGGGTGGGAATATGGGCACTCAAGCCAGATTGCGTCAAGTCCATTCTGCCTCAACTAG  
ATGTCGACAGCTGGGCTTGGGGTGGGAATATGGGCACTCAAGCCAGATTGCGTCAAGTCCATTCTGCCTCAACTAG  
TTAGTGACAGAAATAAAATGAGTTAACATGGAACTTAAAGACTCATACATACTAAAGGGATCAGTAAGTGTAA  
TTGTCAGTGGGCAAATAGGGGACTGTGGATTGAGTGGAAATAGAGAATTATCTGACTTAAATACGGAGATTGTC  
TATCCATGATTGCTGCTCTATAAAGTTGAATCATAAAGCACAGTGTGATGAGACATTGGCTTGGGAGCAGCA  
GGATTCTGGGTTATATCCAGCTGTCGCTCCACAGGTATGTGACTGGACAGGGCACTCACCTTTCATGTTGAGTT  
TCATCAACTATGAAATAAAAGAGACTAGAACATACGCATCTCTAAAGTGTGAAATAGTGTACAAATAGTCA  
ACTTAGCCTGGGCTGTCAGGCATAATAACGCTACCATGTGCTGGCTCAGCTGTGCAAGGGACTCTCTGAACATT  
TGATATGTTCAACTAATTAAATCTTACATTAATTATGAGGTAGGCTTATCACCCACACATCACAGATGAAGAAC  
TATGACATGAAGAGGTTAACGAGTAGCTGTTAACGAGTCAAGCAGAACAGCGGATTGAGGTTGAGCACTC  
TGGCTCCAGAGTCCATCCTCTAAAGCCATGTCAGCTGGTCTCCCTCTAGTGAATATTCACTGCTAGTAACAGAAG  
AAGAGTAGCTAAATAAGAAATTATTTCTCTCACATTAAATAAGATTGGAGGTAGTCGATGAGGCTGTGAGTGG  
CCTCATAAAGTCATGAGACGCCCTGGTCTTTCCAACTCCTTGCATGCCATCCTGGTTCTAGTGTACCCATTCTCGTG  
GTCATGATATGGGCTAGGGCTCCAGCCATCATGACCACATCTAGGCAAGTCAGGAGTAGAAATGAGGAAACAGCAAA  
AGATGTCGGCCATTTCCAGTGCCTCACCTATATTATCAGCGATCCTCACCTGCATGGGCTAGGAAGTGTAA  
CAGGGCTCACACTGCCTGGAGTTCTGCAGTAGGGAGAAAGAATGGGATATTGAGAAAACAACTAACGAATGTTGCT  
GCCACACTGAGGAACCCATGTATGGGCTGCTGAAAAAGGGGGGCAAGGCTGGTACAGTGGCTACGCCGTGAA  
AGTACTTGGGAGGCTAGGTGGCGGATCACTTGAGCTCACAAAGTCAGGACAGCCTGGCAACATGCCAAACCTCG  
TCTTACAAAAAATACAAAAAAATTAAACCGGTGAGTGGCGTGCCTGAGTCCAACTGCTGGGAAGCTGAGGTGG  
AGGATCACTTGAGGCCAGGGCAGAGGTGCACTGAGCTGAGATCATGCCACTGCCCTCACCTGCATGACAGAACATGA  
GATCCTCTCTAAAAATAGAGGGTACCAAGAGATGCAAGGGGGTGAGGGCAGCATGACTACTCTCTGTAGGAGA  
CCTTAACCTCTATAAATGGAGGCCAAATGTTACTGCCATCAAAGCCAGGAATCCTTCTGGAGGCTAACCTCG  
CCCTTCTAATCCCTATCAATCTGGTTCTGAGAATGTGACTGCTAGAAACCCAGGCATATTGTTCTAAGAAC  
ACTTGTTCTGGTAATTACCAACAAAGGGACATCAGAGGATGTGAGGGAGTCTGAATGGTTGATCAACTAAGTGA  
GAGCAGCACAGATGTTGTCAGCTATTGAGAATGTACAGATAAGACCATTTGAAAGTTGTTGCACTGCT  
ATGATCTGTTGTAACATTCTCAAGCGATGTCCTATTCTCTAGGAGGGATAGTAGAAATTATTCAATTAA  
ACCTAGAGAAATATAACCCAAATGACTGAAAGGAAGAAATGTAGAAAAGTATATAAAATAATTGTTGCA  
TTAAAGACATAAAAGTAAATTACTACATAAAATCTAAGTTTCTCAGCTATTGAGCTTAAATATTGTTCTTAA  
CACATTATTAACTGCTGTAACAAACTACCTCACAAATTAGTGGCTTAAAGAAAATTAAATTATTGATGTGGTA  
CATATAATTCTGCTTCTCATTCTACTGCTGATACTGGCTTATGATGGCTCATGATGGCTGGGGCCCTAGCGAGG  
TGTATTGTCGGCATGAGAATGGTTCTGCAACTTGGGTTGGCTGGCTCAGCTAAGCAGTTTGCCTGGAGTCT  
CAGTGCAGTGGAGACAGTGAATGGACTTGAATTACCTGAATGCTCCTCACTCATGTCGGTGTCTGGCTGAGAAC  
TCAAACAGCAGGGCTCTCTCTAATCTCCTCTCCACATGGCTCTCTGCATGACAGCTTAGGGTA  
AGACTTGTCAAGGATGGTCAGAACTCTTACAGTACAGAACAGAGAGAGACAGAGGCCATTACCTTATTAGCCA  
GTCACACAGTACCCACCTCCACCACTCATCTGGCTGTCACAAAGAACCATCCACCTTGTGATGGGGCATGG  
CAAGGTTCTAGGAGAGCACATTCTGTCAGGCAATTCAAGAACACTGCTACACTCCAGAACGATCTGTTGCCTTA  
TTATCATAGCTCTGATTTAATTCTCCAGCAACCCCTAGGAGATTATGAGCTTATTATCCCATTTCAGAGAAA  
TGAAGATTGTTATGGTTAACGTCATCTGCTAATGAGTAGCAGCTGTTCAACCGCAGTTGCTGCA  
ACTCAAGGGCACATGGTGAGCAATCAGAACAGGTGTTAGCTAGCTGCTGACTCTGCAAAACAAAGACTAAGGAGAG  
TTAGCTGATTACCAAAGTGTCCAGTAGACTTCCCCAAATTAGCTGTTAGCTGTTAGCTTGGCAGGACTCATCCCACCTCCT

FIG. 7B (13 of 15)

GTAGCCTGCCAATGTTAAACCTGGGCCTTGAAGTCATCCTGAAACTGATCTATTTACACATGGTGTAAATTGTAAC  
 TGTTAGTTAAGAAGCAATAAAAAATAATAAGGGGTGATATAGATTCTCAGGATTCAAAGGCCATATGCCCTCCCTCT  
 ATTTCTCCCTAAACCGTTAATTCTACACCTTAGCTATCCTATAATTGCTTCATAATTGCTTCATAATGACAAACATAAAAGATAGG  
 TGAAAATCCAGTTAAGGGAGTCTTCAGATTCTGTGTGAGTTAAATCAAGTCCTCTTCTATAGCAGGTAATTCCATG  
 ATGAAGCTGTGGTCTAAGTTATTTGCCTAGGCAGGTAGCTCTCCTGCCACATGCTATCCTCTTCTTGTACT  
 GTCATCCTGAAAATGTGTTAGTGTAAAGAGGATTGATAACAATGTCGGGTATCTCATAACTTAGTCCAATCTGGT  
 ACCACTGTTAGAAAATAATGTAAGCCATATTGATCACCCACGTCTTATTCTATTGAGGATAATATAGTTATTACTAAT  
 TATTGCGTGTAGGTAACATACAGCCATTATTCTGTCCCTTAAGGTTATTGATTGTAAGTCCCTGGTAGAAGAG  
 TACAAACAAAAGGCAAACCTCATCATGTTAAATAACGTGATTCTCTTGGTAGTACCGTACCGTGCAGGAGAC  
 AGGGAAAACACCAAGGTTAACCGTCCACAAGCCAGATAACCATGATGAGTTCTAAAGATTCTCTGTCTTAATGTTCT  
 TCAGTTTGTCATGAGAAGACTGGATATAGCTCTGTTGTTCAATTAGAGGATTATATCTCTTCACACTAGAAAAA  
 TTACCAAGCTGTATCTCTTAAATATTGCTCCCTCATTTCATTTCCATTCCCTGGAGATTCTATTAGATGTTGGGTTGGAT  
 CTTCCTTATATCTCATGTTCTTAACCAATTTCATTTTAAATTTTAAATCTCATGGTAGTTCTGTTGGGTTGGAT  
 CTGTCATACATTACTCTCATTATGCTAGTCTATTATTAACCTTAACTTTCCATTGAGTTTTGTTCTTGT  
 CAACTGCATTTTTTTTTTTTTTGGTAGACAAAGGTCTGGTCTGTACCCAGGCTGGAGTGCAGT  
 GGCATGATTTGGCTCACTGCAACCTCCACCTCCAGGCTCAAGCCATCTTCCACCTCAGTTCCCAAATAGCTGGGAC  
 TGCACTCACCTGCCACATACCCAGCTAAATTATTTGAGAGATGGGTTTGCATGTTGCCAGTCTAGTC  
 TTTAATTGAGCTCAGGCAATCCACCCACCTAGCTCCAAAGTGTGGGATTACAGGCATGAGGCACACACCCAG  
 CCTAGTGAUTGCATTTCCTTTCTAGAAGTTCTGTTGGCTCTTCTGAACCTTCCGGTCTTTTCAATT  
 CCCTGTTATTGTTTATCATGGATTATACCTTATTATTTCTTTCTAGTTACATGATTACTAG  
 GATTTTATACATTATTACCTCTATATTAACCTGGTTTTACATTGTTTATTATCTCTAATTCTTATTGGACTA  
 ATTCTTGTGTTGATGCATCTTAGTTCCCTCGTGGTGGTTCTCATATGGTTGTAATTTTATTGTGAG  
 CTCATCTGGCGAGAGTGGCTCATATGCCCTGATTGAGAATGTGTTCTCCAGAACAACTTATGTTGGCTGAA  
 TCCTAGCAATTCTAGTAATCTGGACTGGCTTTAAGTTATTTCTCACCTTGAAAGCACATACAGTCAGGAATGTACAT  
 TTGTAATTACTATGTTGTCAGCAGCTAGAATTCCATTCTCAATATGACTTTCTTCCATAATGGCCCTAAG  
 CTGATAGCAAGTTTCATTCTGCCTCTGGACATCTGCAGCATTCTCAAAACCCCTTCTCATAGATGGGATAGCTT  
 TCAAGGCTCTGGACGATATGCAGGGCATATCCAGAAATCCCTTGCCCTGGCAAGGCCACATCACTAATTGTTG  
 GAGCTTGAGGCCCTTCCCTCAGGCCATAGACCTATACAGCTTAAACAGCTTAACTTAATGGGAGTCTACTGACAGCTG  
 CCTTGCAACAGCTCTGTGATCTAGCTTGTGATCTTCTCTTCTCTCTGGCACCTGGTGTCCCCCTTCTTCT  
 AACAGCTTGTGTTGCTGACTCTAGCCTCATATGTCAGTACAGCTGGAGGAGGCTGAATGCCATCTGCTCTG  
 ATGTTGCTGTAATACAGTGAATTGAGTTGAGTTGAGTGAACAGCTTCAATTCTGAGTTTCAAGAACAAAATAGAGATAAATGCT  
 TCCATCACTCCTCACAGTGTATCTGGCAAGCATTCTAACATTCTGAGTTTCAAGAACAAAATAGAGATAAATGCT  
 GACTTTTACGGTTGTTGGAAAATTAAACAGATAATGCACTGAAACTTCTGAAACTTCTGAGACATAGCAAGTC  
 AGAGGTTCTCAATTCTGGCTAGGTTGGCTCAGTATCCCCTGGCAACTTTAACATTAGACATTCTGGGCCAGAAGC  
 AATGGCCACACTGTAGTCCCAGCTACCCAGGAGGCTGAGGTAGGAGGATCAGGGGCCAGGAGGCTGAAGTTGCC  
 ATGAGCTGTGATCATGCCACTGCACTCCAGCCTGGGTGATAGAGTGAAGCCCCTGCTCAAAAATAATAAAAGGTA  
 AAAAAAAACAAACACAGAGATTCTGGGTGCTACCCCTCAGCAGTTATGATTCAAGTCTGAGATAGATCCCAGAAA  
 TCTGCATTGAAAGCTCCACAGGTGATCCGATATGCCACCCAGTTGAAACGTTCTTAAAGTTATTGAAAAATCG  
 TAAGTATTCTCATGTTCTCAGATTCTAAGCACTTCAAAGTCATTATTTCTCCACACTGATATTTCATCTCAGATG  
 TGGTGAAGCTGTAGAGAAAACAAGCGTCTCATCAGGCCAGACAGAGGGAAATATCAGCAGGAACCTCAAAGGAAACTATA  
 ACAAGCTAAAGAGAACCTCAGGCCAATGATCGAGCGAAAATTCCAGAAACTGTACAAGCCAAATTCAAGAGTTGAGAGT  
 CAAAAGAGGTAAGAACAGGGCAGAGGGAGCCCTTCTCTGGGATAAAAGAGCAGCGCATGGGCCCTAGCACCTGGGCA  
 TGCTCTGCTGCACCTGGGAGCTGAGAACCTCGAAAGGGTGGAAAGGGGCTCCACAGTCAGAGGGCTACCGAGTGT  
 ATTCTCTGCTCTGCTCTCCCATCCCTGCTCTGACCTCTCCAGACACCTTGGTGTGGTCTTGCCAGGGTAT  
 TCCAGGGCTGAATGATGCCCTGTTGGTTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG  
 GGGTCCAGACCTTCACTTATTGCTGAGTTGTTGTTGACTGATGTCATTCTACTGGGTGATCCACCCCCAAC  
 CTTCTAAAAGGCTAACTGATCTTCTGCTCTGTCAGCTCTCTCTCCCTCTCTCTCTCTCTCTCTCTCT  
 GACTCCTCCACAGATCTAGTTCAAGAACCTGGAGAAGGACTTGTGGTACTTAAAAATGGACATTGCCACCCAGGACTGACTGT  
 GGAGACTGTGGCCCTGCAACCCCTGGAGAAGGACTTGTGGTACTTAAAAATGGACATTGCCACCCAGGACTGACTGT  
 ACACCTCCCTGATGCCAGCACTGGAAAGCTTGGGATCCCAAGGAACCATGAAATTATCCCAAATGGACTCTGACCA  
 ATTTTGCCATACTGGGGGTGGGGATGGAGGATGGTACTCAGGCATGACTGCGTATTATTAAAGTGTGTTTCC  
 ACAATGTAACAAACAAGGCATAAGCAGCTCTCTGCTGACTGGCCAATCACTGCCCCATCTGAGAGATGATTCCCTCTGG  
 CCCATATTGAAATTATTGGAGTAACCTCAAATTGCCCTGAGGAAAATGGAAAATTCCACCAAGTCGATTCAAACGAA  
 TTTCACCTTATAGGAAGGCAGGGCAAACCTGTAGGAGTACGAAACATTCTACAAATCTACAAAGGAAGGCCCTACT  
 ACAATTCCAAAATCATCATGGTGGAAATTGGGAGGAGATTATGTAACCTTACATTAAACATGCAATTAGAAGAATACATTCAAA  
 ACTGATGTTAGGAGATAACCGTACTTGGAGCAGTCAGCCAGAAATCACAGATACTGCTTCACTTAAATGGAAACAATT  
 C

FIG. 7B (14 of 15)

FIG. 7B (15 of 15)

GGAACAATTCCCTCATGTATGGCTCCCTAAAGTGTGGCTGAGCATTGTCCACATGGGTG  
ATGCAAAGGATCACTGAACTAGGAGCAGTTGGAAAAAAATACAATCATGGAAATCCTGTAGC  
ATCGAATGTGCCTACAGGGAGGTAGAAGTATTACATACAACAGTTCTGGTGTCTGTGTA  
GCAACCAGTCAGCCAAAAGGGTTCAGCTGCTGAAATGAGAATGGCTGGATCAAATGGCAGCT  
CATGATTTAAGGATTCTAGTCAGATACCAGACATCCTCACATAGAGAAAATCTGAATGGCTG  
GGGGAGAAGGAGTCAGGAAATGCCCTGGATCTTTCTGGGCTCAAAGTCCCTCTGTGATCA  
TCCTCCAGTATTGGGCAGGACCTGACTGCAGGCATCATGGCCTCTGTGAACTTCTCAAGGGTA  
TGTATTATCTGACAAAAACTACGATGTCCACTAACAGGCCACTGAAAGGTATCTTAGTCAGTTC  
TGCTCATTGCCCAGCCAAGGCCATCGTTTATAACATGATCAAAGATTGCATCTAAATTGT  
GATGATTCCTAAATAATCATTCATTTAGATTTCTATTAAATCCAAGGTATTCTTCAGC  
GGAAATAAGGAAACAGTTACTCTCCACCAAAACCTTGGCCAGTACCATCGACAGAGCATAAGT  
ACCTCTGGCTCCCCCTCTCAACTAGTAACTGAGTTCCAGGTACTTAGCGATTGGTCA  
AGTGCAAAGTGCCAGGGTATGTGCTCTGTGACTGTCAGTCTTACCATCACCACCTCA  
CATTCTCCAGTCACAGATCCTAACTCTGACTGTCAGTCTGGACATCAGACAATATCCCTCT  
CTCTGCCAACCGTACTTAGGGTACATAATAGAACCTTGGAGCTGTGGTTGATGTCTC  
TAGACTAGGTGGGCTTCCAGGTACTCAGTCTCATCCAAATTATGGTICATATTTGGGGGAGAA  
GGGCTAGCCAAAACCTTACACCACTTGTAGTATGCATTTTGGAAAAGCATATTCCAAA  
TCTGAAATGCAAGTTACAGACCTCTTTGTAAATAATTCTTGCTAGTATAATTACAT  
ATAATAAAATTCAACACATTAGGTGTACAATTGGTGAACCTGGCAACTTAGAGTCACCTAA  
CCTTCCTCAGTCAGATATAGAACACTTCTTTATCCCTAAAGCGTCCCCAGCGCGTTTAC  
AATCTCCCTCCCCAGGCCACACCCCTCAACTACGCAATCTCTGACTCACTCTGTCACCATA  
ATTGGTCTCTATCTGGAGCTTCATATCCTGTTACAGTATGTACAAACCTCTTTTGAGACA  
GGGTGTCAGTCTGTCACCCAGCCTGGAGTACAGAGGTGTGATCTCAGTCACTGCAACCTCAAC  
CTCCCAAGGATCAGATGATTCTCTCCACCTCATCCTCCAGTAGCCGGGACTACAGGCGCAT  
GCCACACACCTGGTAATTGGTACTTTGTAGAGACAGGGGTCGCTATGTTGCCAGG  
CTGGTCTGAACTCTGGGCTCAAGCGATCCTCTGCTCAGGCCCTCCAAAGTGTGGGATTAC  
AGTGAGCCACTGCACCTGGGCTTAAACCTTCATTAAACACATTCTCTTAATTGAAGA  
TTGCCTACATTATCAATGCAATTGGTGTGCTGCTATGTGTTATATTGAGC  
ACTAAATGCCAGATGTGCAAGTGAAGATAAAATGACAAATGAGATGGTTGAAACCCAGC  
AGTGAATATTCACTCCTCTGAGAGAGCTCCAGCCCTCTGACTCACTTCTCACACAGCA  
CAGCAGCACTTGTGGTCTGCTTATCTGAAGAGGTTAGGTACTTTGTTCTACT  
TATTACTCGAAACCACCTCTGCCCTAGAAATTGTAACTTCCGCTCAGTTCCGGTAACCG  
CCATTGTCCTGTAACAATTACGCGCCGTGTAATGTGAATCTT

FIG. 7C

hCLASP4	-----MFPMEDISISVIGRQRRTVO-----	20
hCLASP5	-----MTHLNSLDVQLAQELG-----	16
hCLASP3	-----MAERRAFAQKISRTVAAEVRKQIISGQYSGSPQLLKNLNVG	41
hCLASP2	-----MLLFYDDFQTAILRRQGRYICS-----	23
hCLASP7	-----MAASERRAFAHKINRTVAAEVRKQVSRSRSGSPHSSRRCSSSL	43
hCLASP1	MSFRGKVFKEPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN	60
... .		
hCLASP4	-----STVPEDAEKRAQSLFVKECIKYSTDWHVVNYK-----	53
hCLASP5	-----DFT-----	19
hCLASP3	N-----ISHHTTVPLTEAVDPVLEDYLITHPLAVDSGPLRDLIEFP	83
hCLASP2	-----TVPAKAEEEAQSLFVTECIKYNSDWHLVNYK	55
hCLASP7	G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP	79
hCLASP1	DPLQDLLFFPSDDFSAAATVSWDIRTLYSTVPEDAEHKAENLIVKEACKFYSSQWHVVNYK	120
::		
hCLASP4	YEDFSGDFRMLPCKSLRPEKIPNHF <small>E</small> IDEDEDCEKDED-----SSSLCSQKGGVIKG	105
hCLASP5	DDDLDVVFTPKECRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI	63
hCLASP3	PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI	126
hCLASP2	YEDYSGEFRRQLPNKVVKLDKLPVHVVYEVDEEVDKDED-----AASLGSQKGGITKHG	107
hCLASP7	ADDLELLLQPRECRTEP-GIPKD-EKLDDAQVR-----AAVEMYIEDWVI	122
hCLASP1	YEQYSGDIRQLPRAEYKPEKLPHSFEIDHEDADKDEDTTSHSSSKGGGGAGGTGVFKSG	180
:: . :* . ::* .		
hCLASP4	WLHKANVNSTIT--VTMKVFKRRYFYLTLQPDGSYIILNSYKDEKNSKESK-GCIYLDACI	162
hCLASP5	VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHNVLC	118
hCLASP3	VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGSYQDDQDDLKRRMSI	183
hCLASP2	WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYLNLFYKDEKISKEPK-GSIFLDSCM	164
hCLASP7	VHRRYQYLSAAY--SPVTTDTQRERQKG-LPRQVFEQDASGDERSGPEDSNDSRGGSGP	179
hCLASP1	WLYKGNFNSTVNNTVTVRSFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLDSC	239
:: . :* . ::* . : . . .		
hCLASP4	DVVQCPKMRRHAFELKMLDKYSHYLAETEQEMEEWLITLKKIIQINTDSLVQEKKETVE	222
hCLASP5	DVSGKGPVTACDFDLRSLQPDKRLENLLQQVSAEDEFEKQNEARRTN-----RQAE	169
hCLASP3	DDTPRGSWACSFIDLKNSLPDALLPNLLDRTPNNEEIDRQNDQRKSN-----RHKE	234
hCLASP2	GVVQNNKVRRAFELKMQDKSSYLLAADSEVEMEEWITILNKILQLN-----FEAMQEK	219
hCLASP7	EDTPRSGGASSIFDLRNLAADSLLPSSLERAAPEDVDRRNETLRRQH-----RPPA	230
hCLASP1	GVVQNNRLRKYAFELKMNLDITYFVLAAETESDMDEWIHTLNRLQISPEGPLQGRRSTEL	299
*: * : . : : . : . : .		
hCLASP4	TAQDDETSS---QGKAENIMASLERSMHPPELMKYGRETEQLNKLSRGDRQNLFSFDSE	278
hCLASP5	LFFALYPSVD---EEDAVEIRPVPECPKHEHLG-----N-----RILVKLLTLKFEIE	212
hCLASP3	LFALHPSPD---EEEPIERLSPVPDIPKHF-----QRLLVKCLSLKFEIE	277
hCLASP2	RNGDSHEDD---EQSKLEGSGSGLSDSYLPELAKSAREAEIK---LKSESRVKLFLYLDPD	272
hCLASP7	LLTLYPAPD---EDEAVERCSRPEPPREHFG-----QRLIVKCLSLKFEIE	273
hCLASP1	TDLGLDSDLNSVTCECTPEETDSSENNLHADFAKYLTETEDTVKTTRNMERLNLFSLDP	359
. : . : : . : . : . : .		
hCLASP4	VQRLDFS---GIEPDIKP-FEEKCNKRFVLVNCHDLTFNILQIGDNAKGPPTNVEPFFI	333
hCLASP5	IEPLFAS---IALLYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARSASFV	268
hCLASP3	IEPIFAS---LALLYDVKEKKKISENFYFDLNSEQMKGLLRPHVPPAAITTLARSAIFSI	333
hCLASP2	AQKLDFS---SAEPEVKS-FEEKFGKRLVVKCNDLSFNLQCCVAENEEGPTTNVEPFFV	327
hCLASP7	IEPIFGI---LALLYDVREKKKISENFYFDLNDSMKGLLRAHGTHPAISTLARSAIFSV	329
hCLASP1	IDTLKLQKKDLLEPESVIKPFEKAKRIMIICKALNSNLQGCVTENENDPITNIEPFFV	419
: : . : . : . : . : . : * :		

FIG. 8 (1 of 6)

FIG. 8 (2 of 6)

FIG. 8 (3 of 6)

FIG. 8 (4 of 6)

FIG. 8 (5 of 6)

hCLASP4 hCLASP5 hCLASP3 hCLASP2 hCLASP7 hCLASP1	<b>ITAM</b> EKGTEENVKIIQDSDKVNAKEELDPKYAHIQVTVKPFDDKELTERKTEFERNHNISRFV 1799 QCAGAEFVEVIKDKSTPVDTKLDPNKAYIQITFVEPYFDEYEMKDRVTYFEKNFNLRRFM 1810 ERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITKVEPYFDTYEMKDRITYFDKNYNLRRFM 1932 DKFGSENVKMIQDSGKVNPKDLSKYAYIQVTVHVLFFFDEKEQERKTEFERSHNIRRFM 1770 ERFGDDVVEIIKDSYPVDKSKLDOKAYIQITFVEPYFDTYELKDRVTFDRNYGLRTFL 1851 DKFGADNVKIIQDSNKVNPKDLSKYAYIQVTVTFFEEKEIEDRKTDFFEMHHNINRFV 1972 : ** : *::*:** *: . **.: *::*: *: *: *: *: *: . : *
hCLASP4 hCLASP5 hCLASP3 hCLASP2 hCLASP7 hCLASP1	<b>ITAM</b> ITAM DOCK motif FEAPYTLGKKQGCIEEQCKRRTIITTSNSFPYVKKRIPINCEQQINLKPIDGATDEIKD 1859 YTPFTLEGRPRGELHEQYRRNTVLTMMHAFPYIKTRISVIQKEEFVLTPIEVAIEDMKK 1870 YCTPFTLDGRAHTELHEQFQRKTIITTSASHFPYIKTRVNTHKEEIIITPIEVAIEDMQK 1992 FEMPFQTGKROGGVEEQCKRRTIITAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSK 1830 FCTPFTPDGRAHTELPEQHKRKTLSTDHAFPYIKTRIRVCHEETVLTTPVEVAIEDMQK 1911 FETPFTLSGKKHGGVAEQCKRRTIITTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSR 2032 : *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *
hCLASP4 hCLASP5 hCLASP3 hCLASP2 hCLASP7 hCLASP1	<b>Coiled-coil</b> KTAELQKLCSSSTDVDMIQLQLKLGWVSVQVNAAGPLAYARAFLNDSQASKYPPKKVSELK 1919 KTLQLAVAINQEPPDAKMLQMVLSQGSVGATVNQGPLEVAQVFLAEIIPADPKLYRHHNKL 1930 KTQELAFATHQDPADPKMLQMVLSQGSVGTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKL 2052 KVAELRQLCSSAEVDMIKLQLKLGWSVSVQVNAAGPLAYARAFLDDTNKRYPDNKVKLLK 1890 KTRELAFATEQDPPDAKMLQMVLSQGSVGPTVNQGPLEVAQVFLAEIIPEDPKLFRHHNKL 1971 KVSELNQLCTMEEVDMISLQLKLGWSVSKVNAAGPMAYARAFLEETNAKKYPDNQVKLLK 2092 *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *
hCLASP4 hCLASP5 hCLASP3 hCLASP2 hCLASP7 hCLASP1	<b>Coiled-coil</b> DMFRKFIQACSIALELNERLIKEDQVEYHEGLKSFRDMVKELSDIIHEQILQEDTMHSP 1979 LCFKEFIMRCGEAVEVKNRKLTADQREYQQEELKKNNKLKENLRPMTERKIPELYKFIFR 1990 LCFKDFTKRCEDALRKNKSLIGPVQKEYQRELGKLSSP----- 2090 EVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKESELIMHEQICPLEEKS- 1949 LCFKDFCKCEDALRKNKALIGPDQKEYHRELERNYCRRLREALQPLLTQRLPQLMAPTP- 2030 EIFRQFADACGQALDVNERLIKEDQLEYQEELRSHYKDMSELSTVNEQITGRDDLSKR 2152 *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *
hCLASP4 hCLASP5 hCLASP3 hCLASP2 hCLASP7 hCLASP1	<b>PDZ ligand</b> WMSNTLHVFCIAISGTSSDRGYGSPPR <del>YAEV</del> -- 2008 VESQKRDSFHRSSFRKCETQLSQGS----- 2015 ----- VLPNSLHIFNAISGTPSTMVHGMTSS <del>SSVV</del> 1980 --PGLRNSLNRASFRKADL----- 2047 GVDQTCTRISKATPALPTVSISS <del>SAEV</del> -- 2180

FIG. 8 (6 of 6)